

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 15:36:11 ; Search time 1125 Seconds
(without alignments)
10761.217 Million cell updates/sec

Title: US-10-813-588-1

Perfect score: 1464

Sequence: 1 atgacatctaagaattatcc.....caagtgatggcagggttaa 1464

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA Main:
1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq.*
4: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq.*
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7: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq.*
8: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq.*
9: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1464	100.0	1464	9	US-10-813-588-1
2	1464	100.0	1464	9	US-10-813-588-5
3	1464	100.0	1464	9	US-10-813-588-3
4	1464	100.0	1464	9	US-10-813-588-7
5	1462.4	99.9	1761	6	US-10-295-027-1083
6	1462.4	99.9	2010	6	US-10-295-027-1082
7	1462.4	99.9	2010	8	US-10-783-528-23
8	1462.4	99.9	2010	8	US-10-783-528-24
9	1459.8	99.7	2145	3	US-09-759-1308-72
10	1459.8	99.7	2145	7	US-10-741-790-72
11	1459.8	99.7	2888	7	US-10-312-352-47
12	1459.8	99.7	3151	5	US-10-003-132-1
13	1459.8	99.7	3594	3	US-09-759-1308-71
14	1459.8	99.7	3594	7	US-10-741-790-71
15	1459.8	99.7	3676	3	US-09-814-353-20367
16	1440.2	98.4	2547	6	US-10-108-260A-999
17	1107.4	75.6	2310	6	US-10-295-027-1084
18	1040.6	71.1	2145	5	US-10-003-132-12
19	584.2	39.9	2473	6	US-10-108-260A-2375
20	565.6	38.6	636	7	US-10-138-588-71
21	564.2	38.5	1538	7	US-10-138-588-69
22	548	37.4	596	8	US-10-696-639-1823
23	451.4	30.8	2836	5	US-10-003-132-3

Sequence 43, Appli
Sequence 19131, A
Sequence 1822, Ap
Sequence 13, Appli
Sequence 5, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 861, App
Sequence 6505, Ap
Sequence 1113, Ap
Sequence 2, Appli
Sequence 13, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 96, Appli
Sequence 65, Appli
Sequence 1947, Ap

24 449.8 30.7 1871 3 US-09-823-038A-43
25 414.4 28.3 456 3 US-09-918-995-19131
26 400 27.3 400 8 US-10-696-639-1822
27 368.2 25.2 1509 5 US-10-003-132-13
28 223 15.2 2868 6 US-10-003-132-5
29 205.8 14.1 2310 6 US-10-191-436-4
30 205.8 14.1 2310 6 US-10-191-436-6
31 205.8 14.1 2310 10 US-11-055-679-4
32 205.8 14.1 2310 10 US-11-055-679-6
33 205.6 14.0 2020 6 US-10-094-749-861
34 205.6 14.0 6595 8 US-10-723-860-6505
35 204 13.9 1962 5 US-10-060-830-1113
36 204 13.9 2190 5 US-10-060-830-2
37 204 13.9 2200 7 US-10-451-010-13
38 204 13.9 2280 5 US-10-060-830-1
39 204 13.9 2328 6 US-10-191-436-1
40 204 13.9 2328 6 US-10-191-436-3
41 204 13.9 2328 10 US-11-055-679-1
42 204 13.9 2328 3 US-09-974-298-96
43 204 13.9 5657 3 US-10-084-817-65
44 204 13.9 5657 5 US-10-106-698-1947
45 201.6 13.8 2428 5 US-10-106-698-1947

ALIGNMENTS

RESULT 1

US-10-813-588-1
; Sequence 1, Application US/10813588
; Publication No. US20050053969A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0071-USA
; CURRENT APPLICATION NUMBER: US/10/813,588
; CURRENT FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: US/09/691,344
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/183,583
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-813-588-1

Query Match 100.0%; Score 1464; DB 9; Length 1464;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACATCTAAGAAATTTATCCGGGACCTACCCCAATCACACTGTTTGGGAAAGACAATT 60
|||||
DB 1 ATGACATCTAAGAAATTTATCCGGGACCTACCCCAATCACACTGTTTGGGAAAGACAATT 60
|||||
QY 61 ACAGTACCAAGGGGAAAGACTGATTTCTGAGTTGGGAGATTGATATCGAATCCCAG 120
|||||
DB 61 ACAGTACCAAGGGGAAAGACTGATTTCTGAGTTGGGAGATTGATATCGAATCCCAG 120
|||||
QY 121 ACCTGTGCTTCTGACTATCTTCTTCCAGCTCTTCAGATCAATATGTCATCATCTGT 180
|||||
DB 121 ACCTGTGCTTCTGACTATCTTCTTCCAGCTCTTCAGATCAATATGTCATCATCTGT 180
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BEST AVAILABLE COPY

Res 9, 10, 13, 14

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QY 181 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTGAACACAAGTGAAGTAACCGTCCGCTTT 240
Db 181 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTGAACACAAGTGAAGTAACCGTCCGCTTT 240
QY 241 GAGAGTGGATCCACATCTTTCGCGGGGTTTTTGTGCTGACCTATCGGAGCGACCAAT 300
Db 241 GAGAGTGGATCCACATCTTTCGCGGGGTTTTTGTGCTGACCTATCGGAGCGACCAAT 300
QY 301 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTAATTTGAAGACAGAAATACAGCAA 360
Db 301 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTAATTTGAAGACAGAAATACAGCAA 360
QY 361 TTCTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 420
Db 361 TTCTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 420
QY 421 TATAGATACCTCTTTATTTGTCNAAGCTGCCATCATGTCAGGAATATTCGTGATGA 480
Db 421 TATAGATACCTCTTTATTTGTCNAAGCTGCCATCATGTCAGGAATATTTGCTGATGA 480
QY 481 CTAGGTGGCCAGATCAGTGTGCTTCAGCGCAAGAGGATCAGTGCATATGAAGGGATTCTG 540
Db 481 CTAGGTGGCCAGATCAGTGTGCTTCAGCGCAAGAGGATCAGTGCATATGAAGGGATTCTG 540
QY 541 GCCAATGGTGTCTTCGAGGGATGGTTCCTGTGAGCAAGCGATTTCTGTTTACCTCC 600
Db 541 GCCAATGGTGTCTTCGAGGGATGGTTCCTGTGAGCAAGCGATTTCTGTTTACCTCC 600
QY 601 AATGGTTCGAGCAGATCTTGAATTTTGAACCTGACGGCAATTCAGAGCTTCTTCTCA 660
Db 601 AATGGTTCGAGCAGATCTTGAATTTTGAACCTGACGGCAATTCAGAGCTTCTTCTCA 660
QY 661 TGCGAGTCGCTCAATGAGAGTGGAGACCAAGTTTCACTGTCTCTGCGCAAGCCGCACT 720
Db 661 TGCGAGTCGCTCAATGAGAGTGGAGACCAAGTTTCACTGTCTCTGCGCAAGCCGCACT 720
QY 721 CAGGACCAAGGCCCATCATGGCTTCGGCGCAGTAGAGCAACCAACCAAGCCAGGAG 780
Db 721 CAGGACCAAGGCCCATCATGGCTTCGGCGCAGTAGAGCAACCAACCAAGCCAGGAG 780
QY 781 TGCTGGAGATCGATTTGGGGGAGAAAGAAATACAGGAATTAGGACCAAGGATCT 840
Db 781 TGCTGGAGATCGATTTGGGGGAGAAAGAAATACAGGAATTAGGACCAAGGATCT 840
QY 841 ACACAGTCGAATCTCAACTTTTATGTTAAGGTTTTGTGATGAATTTCAAAAAACAATAAT 900
Db 841 ACACAGTCGAATCTCAACTTTTATGTTAAGGTTTTGTGATGAATTTCAAAAAACAATAAT 900
QY 901 TCTAAGTGGAGACCTATAAGGAATTTGTAATTAATGAAGAAAGGTGTTTCAGGGTAAC 960
Db 901 TCTAAGTGGAGACCTATAAGGAATTTGTAATTAATGAAGAAAGGTGTTTCAGGGTAAC 960
QY 961 TCTAACTTTTCGGGACCCAGTGCAAAACAATTTTCATCCCTCCATCGTGGCCAGATATGT 1020
Db 961 TCTAACTTTTCGGGACCCAGTGCAAAACAATTTTCATCCCTCCATCGTGGCCAGATATGT 1020
QY 1021 CGGGTGTCTCCCAAGACATGCAACAGAGGATAGCTTTGAAGGTGGAGCTCATTTGGTTGC 1080
Db 1021 CGGGTGTCTCCCAAGACATGCAACAGAGGATAGCTTTGAAGGTGGAGCTCATTTGGTTGC 1080
QY 1081 CAGATTACAGAGTAATGATTCATTTGGTGTGGCGCAAGCAAGTCAAGCACCAGTGT 1140
Db 1081 CAGATTACAGAGTAATGATTCATTTGGTGTGGCGCAAGCAAGTCAAGCACCAGTGT 1140
QY 1141 TCAACTAAGAAAGAAAGTGAACAATCACAAGGCCCATCCCTCGGAAGAAACATCCACA 1200
Db 1141 TCAACTAAGAAAGAAAGTGAACAATCACAAGGCCCATCCCTCGGAAGAAACATCCACA 1200
QY 1201 GGAATAAACATTAACAAGTGGCTTATTCATTTGGTGTCTCTTGTGCTCTGCTGTTGCT 1260
Db 1201 GGAATAAACATTAACAAGTGGCTTATTCATTTGGTGTCTCTTGTGCTCTGCTGTTGCT 1260
QY 1261 GGAATGGGATCTTTGACGCTTTAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1320
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Db 1261 GGAATGGGATCTTTGACGCTTTAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1320
QY 1321 GCGGAGGCTCAGAAAACAGACTGTTTGAAGCAGATTTAAATATCCCTTTGCCAGACATCAG 1380
Db 1321 GCGGAGGCTCAGAAAACAGACTGTTTGAAGCAGATTTAAATATCCCTTTGCCAGACATCAG 1380
QY 1381 TCAGCTGAGTTCACCATCAGCTATGATAATGAAGAGGAGATGACACAAAAGTTAGATCTC 1440
Db 1381 TCAGCTGAGTTCACCATCAGCTATGATAATGAAGAGGAGATGACACAAAAGTTAGATCTC 1440
QY 1441 ATCACAAGTGATATGCGCAGTTAA 1464
Db 1441 ATCACAAGTGATATGCGCAGTTAA 1464
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RESULT 2

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US-10-813-588-5
; Sequence 5, Application US/10813588
; Publication No. US20050053969A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0071-USA
; CURRENT APPLICATION NUMBER: US/10/813,588
; CURRENT FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: US/09/691,344
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/183,583
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-813-588-5
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Query Match 100.0%; Score 1464; DB 9; Length 1620;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 157 ATGACATCTAAGAATATTATCCCGGAGCTACCCCAATCACACTGTTTTCGCAAAAGACAATT 216
QY 61 ACAGTACCAAGGGGAAAGACTGATTCCTGAGGTGGGAGATTTGGATATCGAATCCAG 120
Db 217 ACAGTACCAAGGGGAAAGACTGATTCCTGAGGTGGGAGATTTGGATATCGAATCCAG 276
QY 121 ACCTGTGCTCTGACTATCTTCTTCCACAGCTCTTTCAGATCAATATGGTCCATCTGT 180
Db 277 ACCTGTGCTCTGACTATCTTCTTCCACAGCTCTTTCAGATCAATATGGTCCATCTGT 336
QY 181 GGAAGTATGATGTTTCCCAAGAACTCTTGTGTAACAACAAGTGAAGTAAACGTCGCTTT 240
Db 337 GGAAGTATGATGTTTCCCAAGAACTCTTGTGTAACAACAAGTGAAGTAAACGTCGCTTT 396
QY 241 GAGAGTGGATCCCAATTTCTGCGCGGGTTTTTGTGCTGACCTATGCGAGCAGGACCAT 300
Db 397 GAGAGTGGATCCCAATTTCTGCGCGGGTTTTTGTGCTGACCTATGCGAGCAGGACCAT 456
QY 301 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTAATTTGAAGACAGAAATACAGCAA 360
Db 457 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTAATTTGAAGACAGAAATACAGCAA 516
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9, 10, 13, 14
for 9

QY 361 TTCTGCCAGCTGGTTGTAGACGCTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 420
DB 517 TTCTGCCAGCTGGTTGTAGACGCTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 576
QY 421 TATAGATACCTCTTTATTTGTGCAAGCTGCCATCGCAGGAATAATTTGCTGATGAA 480
DB 577 TATAGATACCTCTTTATTTGTGCAAGCTGCCATCGCAGGAATAATTTGCTGATGAA 636
QY 481 CTAGGTGGCAGATCAGTGTCTTACGCGCAAGGAGATCAGTCGATATGAAGGATTCG 540
DB 637 CTAGGTGGCAGATCAGTGTCTTACGCGCAAGGAGATCAGTCGATATGAAGGATTCG 696
QY 541 GCCAATGGTGTCTTTTCGAGGATGTTCTCTCGACAGCGATTTCTGTTTACCTCC 600
DB 697 GCCAATGGTGTCTTTTCGAGGATGTTCTCTCGACAGCGATTTCTGTTTACCTCC 756
QY 601 AATGGTTGACGAGATCCTTGAATTTGAACTGACGGGCAATACAGAGCTTTCTCTCA 660
DB 757 AATGGTTGACGAGATCCTTGAATTTGAACTGACGGGCAATACAGAGCTTTCTCTCA 816
QY 661 TGGCAGTTCGTCATCAGAGTGAGACCAAGTTTCACTGTCTCTGCGCAAGCCGACTT 720
DB 817 TGGCAGTTCGTCATCAGAGTGAGACCAAGTTTCACTGTCTCTGCGCAAGCCGACTT 876
QY 721 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAAAACACCAAAACCCAGAG 780
DB 877 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAAAACACCAAAACCCAGAG 936
QY 781 TGGCTGGAGATCGAATTTGGGGAGAAAAAGAAATACAGGAATTAGGACCAAGATCT 840
DB 937 TGGCTGGAGATCGAATTTGGGGAGAAAAAGAAATACAGGAATTAGGACCAAGATCT 996
QY 841 ACACAGTCGAATTTCACTTTATGTTTAAAGGATTTGTGATGAATTTCAAAACATAT 900
DB 997 ACACAGTCGAATTTCACTTTATGTTTAAAGGATTTGTGATGAATTTCAAAACATAT 1056
QY 901 TCTAAGTGAAGACCTATAAGGAATGTGAATAATCAAGAAAGGTGTTTCAGGGTAAC 960
DB 1057 TCTAAGTGAAGACCTATAAGGAATGTGAATAATCAAGAAAGGTGTTTCAGGGTAAC 1116
QY 961 TCTAAGTGAAGACCTATAAGGAATGTGAATAATCAAGAAAGGTGTTTCAGGGTAAC 1020
DB 1117 TCTAAGTGAAGACCTATAAGGAATGTGAATAATCAAGAAAGGTGTTTCAGGGTAAC 1176
QY 1021 CGGGTTGTCCTCCAGACATGGCACAGAGATAGCTTGAAGTGGAGCTCATTTGGTTC 1080
DB 1177 CGGGTTGTCCTCCAGACATGGCACAGAGATAGCTTGAAGTGGAGCTCATTTGGTTC 1236
QY 1081 CAGATTACCAAGGATTAATGATTCATTTGGTGTGGCGCAAGTCAAAAGCAGCTGTT 1140
DB 1237 CAGATTACCAAGGATTAATGATTCATTTGGTGTGGCGCAAGTCAAAAGCAGCTGTT 1296
QY 1141 TCACTTAAGAAAGAGATGAGCAATCAAGGCCCATCCCTCGGAAGAAACATCCACA 1200
DB 1297 TCACTTAAGAAAGAGATGAGCAATCAAGGCCCATCCCTCGGAAGAAACATCCACA 1356
QY 1201 GGAATAAACATTTACAGAGTGGCTATTCATTTGGTGTCTCTGTTGTTCTGTTGTT 1260
DB 1357 GGAATAAACATTTACAGAGTGGCTATTCATTTGGTGTCTCTGTTGTTCTGTTGTT 1416
QY 1261 GGAATGGGGATCTTTTCAGCTTTAGAAAGAAAGAAAGTCCGTATGATCA 1320
DB 1417 GGAATGGGGATCTTTTCAGCTTTAGAAAGAAAGAAAGTCCGTATGATCA 1476
QY 1321 GCGGAGCTCAGAAAAACAGACTGTTGGAAGCAGATTAATAATCCCTTTGCCAGACATCAG 1380
DB 1477 GCGGAGCTCAGAAAAACAGACTGTTGGAAGCAGATTAATAATCCCTTTGCCAGACATCAG 1536
QY 1381 TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAGTTAGATCTC 1440
DB 1537 TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAGTTAGATCTC 1596

QY 1441 ATCAAGATGATATGCGAGTTAA 1464
DB 1597 ATCAAGATGATATGCGAGTTAA 1620
RESULT 3
US-10-813-588-3
; Sequence 3, Application US/10813588
; Publication No. US20050053969A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0071-USA
; CURRENT APPLICATION NUMBER: US/10/813,588
; CURRENT FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: US/09/691,344
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/183,583
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-813-588-3

Query Match 100.0%; Score 1464; DB 9; Length 1761;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCAGACTGTTTGGGAAAGACAAT 60
DB 298 ATGACATCTAAGAAATATATCCCGGACCTACCCCAATCAGACTGTTTGGGAAAGACAAT 357
QY 61 ACAGTACCAAGAGGGAAGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCCAG 120
DB 358 ACAGTACCAAGAGGGAAGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCCAG 417
QY 121 ACCTGTGCTTCGACTATCTTCTTCCAGCTCTTTCAGATCAATATGCTCCATCTGT 180
DB 418 ACCTGTGCTTCGACTATCTTCTTCCAGCTCTTTCAGATCAATATGCTCCATCTGT 477
QY 181 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTAACAGAGTGAAGTAAACCGTCCGCTTT 240
DB 478 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTAACAGAGTGAAGTAAACCGTCCGCTTT 537
QY 241 GAGAGTGAATCCCAATTTCTGCGGGGTTTTTGTGACCTATTCGAGAGCAGCAGCAT 300
DB 538 GAGAGTGAATCCCAATTTCTGCGGGGTTTTTGTGACCTATTCGAGAGCAGCAGCAT 597
QY 301 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTATTGGAAGACAGAAATACAGCAAA 360
DB 598 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTATTGGAAGACAGAAATACAGCAAA 657
QY 361 TTCTGCCAGCTGGTTGTAGACGCTAGCAGGAGACATTTCTGGGATATGTTAGATGA 420
DB 658 TTCTGCCAGCTGGTTGTAGACGCTAGCAGGAGACATTTCTGGGATATGTTAGATGA 717
QY 421 TATAGATACCTCTTTATTTGTGCAAGCTGCCATCGCAGGAATAATTTGCTGATGAA 480
DB 718 TATAGATACCTCTTTATTTGTGCAAGCTGCCATCGCAGGAATAATTTGCTGATGAA 777
QY 481 CTAGGTGGCAGATCAGTGTGCTTTCAGCGCAAGGAGATCAGTCGATATGAAGGATTCG 540


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Db      838  GCCAATGGTGTCTTTTCGAGGATGGTTCCTGTGACAGCGATTTCTGTTCCTCC 997
Qy      601  AATGGTTGACGAGATCCTTGTAGTTTGAACCTGACGGGCAATCAGAGCTTCTCTCA 660
Db      898  AATGGTTGACGAGATCCTTGTAGTTTGAACCTGACGGGCAATCAGAGCTTCTCTCA 957
Qy      661  TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTCACTGTCTCTGCGCAAGCCGACTT 720
Db      958  TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTCACTGTCTCTGCGCAAGCCGACTT 1017
Qy      721  CAGGACCAAGGCCCATATGGGCTTCGGGCGACAGTAGCAACACACACACAGAG 780
Db      1018  CAGGACCAAGGCCCATATGGGCTTCGGGCGACAGTAGCAACACACACACAGAG 1077
Qy      781  TGGCTGGAGATCGATTTGGGGGAGAAAAGAAATAACAGGAATTAGGACCAAGATCT 840
Db      1078  TGGCTGGAGATCGATTTGGGGGAGAAAAGAAATAACAGGAATTAGGACCAAGATCT 1137
Qy      841  ACACAGTCGAATCTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAAAATAAT 900
Db      1138  ACACAGTCGAATCTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAAAATAAT 1197
Qy      901  TCTAAGTGGAGACCTATAAGGAATTGCAATAATGAAGAAAAGTGTTCAGGGTAAC 960
Db      1198  TCTAAGTGGAGACCTATAAGGAATTGCAATAATGAAGAAAAGTGTTCAGGGTAAC 1257
Qy      961  TCTAATCTTTCGGGACCCAGTGCAAAACAAATTTTCATCCTCCCTCCATCGTGGCAGATGTG 1020
Db      1258  TCTAATCTTTCGGGACCCAGTGCAAAACAAATTTTCATCCTCCCTCCATCGTGGCAGATGTG 1317
Qy      1021  CGGGTGTGTCCTCCCGACATGCGCACGAGATAGCCTTTGAAGGTGGAGCTCATTTGGTTC 1080
Db      1318  CGGGTGTGTCCTCCCGACATGCGCACGAGATAGCCTTTGAAGGTGGAGCTCATTTGGTTC 1377
Qy      1081  CAGATTACAGAGTAATGATTCATTGGTGTGGGCGAAGCAAGTCAAGCAACAGTGT 1140
Db      1378  CAGATTACAGAGTAATGATTCATTGGTGTGGGCGAAGCAAGTCAAGCAACAGTGT 1437
Qy      1141  TCAACTAAGAAAGAAATGAGACAAATCAACAGGCCCATCCCTCGGAAGAAACATCCACA 1200
Db      1438  TCAACTAAGAAAGAAATGAGACAAATCAACAGGCCCATCCCTCGGAAGAAACATCCACA 1497
Qy      1201  GGAATAAACATTACAAACGGTGGCTATTCCATTGGTGTCTCTTGTGTCTGGTGTGCT 1260
Db      1498  GGAATAAACATTACAAACGGTGGCTATTCCATTGGTGTCTCTTGTGTCTGGTGTGCT 1557
Qy      1261  GGAATGGGGATCTTTGACGCTTTAGAAAGAGAGAAAGAAAGAAAGTCCGTATGGATCA 1320
Db      1558  GGAATGGGGATCTTTGACGCTTTAGAAAGAGAGAAAGAAAGAAAGTCCGTATGGATCA 1617
Qy      1321  GCGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAATATCCCTTTGCGACACATCAG 1380
Db      1618  GCGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAATATCCCTTTGCGACACATCAG 1677
Qy      1381  TCAGCTGAGTTTACCATCAGCTATGATAATGAGAGGAGATGACACAAAAAGTTAGATCTC 1440
Db      1678  TCAGCTGAGTTTACCATCAGCTATGATAATGAGAGGAGATGACACAAAAAGTTAGATCTC 1737
Qy      1441  ATCAAGTGTATGGCAGGTAA 1464
Db      1738  ATCAAGTGTATGGCAGGTAA 1761
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RESULT 6

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US-10-295-027-1082
; Sequence 1082, Application US/10295027
; Publication No. US2003023250A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natesha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
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; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1082
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-1082
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Query Match 99.9%; Score 1462.4; DB 6; Length 2010;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTCGGAAGACAATT 60
Db      282  ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTCGGAAGACAATT 341
Qy      61  ACAGTACCAAGGGGAAAGACGTATTCTGAGGTTGGGAGATTTGGATATCGAATCCCGAG 120
Db      342  ACAGTACCAAGGGGAAAGACGTATTCTGAGGTTGGGAGATTTGGATATCGAATCCCGAG 401
Qy      121  ACCTGTGCTTCTGACTATCTTCTTCCACGAGCTTTCAGATCAATATGTTCCATCTGT 180
Db      402  ACCTGTGCTTCTGACTATCTTCTTCCACGAGCTTTCAGATCAATATGTTCCATCTGT 461
Qy      181  GGAAGTATGACTGTTCCCAAGAACTCTGTTGAAACACAAAGTGAAGTAAACCGTCCGCTT 240
Db      462  GGAAGTATGACTGTTCCCAAGAACTCTGTTGAAACACAAAGTGAAGTAAACCGTCCGCTT 521
Qy      241  GAGAGTGGATCCCAATTTCTGCGCGGGTTCCTGTCACCTATGCGAGCAGGACCAT 300
Db      522  GAGAGTGGATCCCAATTTCTGCGCGGGTTCCTGTCACCTATGCGAGCAGGACCAT 581
Qy      301  CCAGATTAAATAACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACAGCAA 360
Db      582  CCAGATTAAATAACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACAGCAA 641
Qy      361  TTCTGCCAGCTGGTTGTAGAGAGCTAGAGAGAGACATTTCTGGGAATATGGTAGATGGA 420
Db      642  TTCTGCCAGCTGGTTGTAGAGAGCTAGAGAGAGACATTTCTGGGAATATGGTAGATGGA 701
Qy      421  TATAGAGATACCTCTTTTATTGTCAGAAAGCTGCCATCCATCGAGGAATAATTGCTGATGAA 480
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Db	702	TATAGAGATACCTCTTTATTGTGCAAGCTGCCATCCATGCAGGAATAATTTGCTGATGAA	761
Qy	481	CTAGGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGATCAGTCGATATGAAGGATTTCTG	540
Db	762	CTAGGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGATCAGTCGATATGAAGGATTTCTG	821
Qy	541	GCCAAATGGTGTCTTTTCGAGGGATGGTTCCCTGTGCAGAAAGCGATTTCTGTTTACCTCC	600
Db	822	GCCAAATGGTGTCTTTTCGAGGGATGGTTCCCTGTGCAGAAAGCGATTTCTGTTTACCTCC	881
Qy	601	AATGGTTGCACGAGATCCTTCAGTATTTGAACTTCAGCGGCAAAATCAGAGCTTCTTCCCTCA	660
Db	882	AATGGTTGCACGAGATCCTTCAGTATTTGAACTTCAGCGGCAAAATCAGAGCTTCTTCCCTCA	941
Qy	661	TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTCACTGGTCTCTCGGCCAAGCCCGACTT	720
Db	942	TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTCACTGGTCTCTCGGCCAAGCCCGACTT	1001
Qy	721	CAGAACCAAGGCCCATCATNGGGCTTCGGGCGACAGTAGCAACAACCAAAACACAGAGAG	780
Db	1002	CAGAACCAAGGCCCATCATNGGGCTTCGGGCGACAGTAGCAACAACCAAAACACAGAGAG	1061
Qy	781	TGGCTGGAGATCGAATTTGGGGGAGAAAAGAAATAACAGGAATTAGGACCAAGGATCT	840
Db	1062	TGGCTGGAGATCGAATTTGGGGGAGAAAAGAAATAACAGGAATTAGGACCAAGGATCT	1121
Qy	841	ACACAGTCGAACTTCAACTTTATGTATTAAGAGTTTTGTGATGAACCTTCAAAAAACAATAAT	900
Db	1122	ACACAGTCGAACTTCAACTTTATGTATTAAGAGTTTTGTGATGAACCTTCAAAAAACAATAAT	1181
Qy	901	TCTAAGTGGAAAGACCTATAAAGGAATTTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC	960
Db	1182	TCTAAGTGGAAAGACCTATAAAGGAATTTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC	1241
Qy	961	TCTAACTTTTCGGGACCCAGTGCAAAACAATTTTCATCCTCCCACTCGGGCCAGATATGTG	1020
Db	1242	TCTAACTTTTCGGGACCCAGTGCAAAACAATTTTCATCCTCCCACTCGGGCCAGATATGTG	1301
Qy	1021	CGGGTTGTCCCCAGACATGGCACAGAGATAGCCTTTGAAGGTGGAGCTCATTTGGTTGC	1080
Db	1302	CGGGTTGTCCCCAGACATGGCACAGAGATAGCCTTTGAAGGTGGAGCTCATTTGGTTGC	1361
Qy	1081	CAGATTACAAAGTAAATGATTTCAATGGTGTGGCGCAAGCAAGTCAAAAGCACAGTGT	1140
Db	1362	CAGATTACAAAGTAAATGATTTCAATGGTGTGGCGCAAGCAAGTCAAAAGCACAGTGT	1421
Qy	1141	TCAACTAAGAAGAAGATGAGACAATCACAAAGGCCCATCCCTCGGAAGAAACATCCACA	1200
Db	1422	TCAACTAAGAAGAAGATGAGACAATCACAAAGGCCCATCCCTCGGAAGAAACATCCACA	1481
Qy	1201	GGAAATAACATTACAACGGTGGCTATTTCCATTTGGTGTCTCTTGTGTCTCTGGTGTGTGCT	1260
Db	1482	GGAAATAACATTACAACGGTGGCTATTTCCATTTGGTGTCTCTTGTGTCTCTGGTGTGTGCT	1541
Qy	1261	GGAAATGGGGATCTTTTGCAGCCTTTAGAAAAGAAAGAAAGAAAGGAAGTCGTTAGATCA	1320
Db	1542	GGAAATGGGGATCTTTTGCAGCCTTTAGAAAAGAAAGAAAGAAAGGAAGTCGTTAGATCA	1601
Qy	1321	GCAGAGCTCAGAAAACAGACTGTTGGAGCAGATTAATAATCCCTTTGCCAGACATCAG	1380
Db	1602	GCAGAGCTCAGAAAACAGACTGTTGGAGCAGATTAATAATCCCTTTGCCAGACATCAG	1661
Qy	1381	TCAGCTGAGTTTACCATCAGCTATGATAATGAGAAGGAGATGACACAAAAAGTTAGATCTC	1440
Db	1662	TCAGCTGAGTTTACCATCAGCTATGATAATGAGAAGGAGATGACACAAAAAGTTAGATCTC	1721
Qy	1441	ATCAAAAGTGNATGGCAGGTTAA	1464
Db	1722	ATCAAAAGTGNATGGCAGGTTAA	1745

RESULT 7

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US-10-783-528-23
; Sequence 23, Application US/10783528
; Publication No. US20040219579A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataeha
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
; FILE REFERENCE: 05882.0191.NPUS01
; CURRENT APPLICATION NUMBER: US/10/783,528
; CURRENT FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-783-528-23

Query Match          99.9%; Score 1462.4; DB 8; Length 2010;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGACATCTAAGAAATTATCCCGGACCTACCCCAATCACACTGTTGCGAAAAAGACAATT 60
Db 282 ATGACATCTAAGAAATTATCCCGGACCTACCCCAATCACACTGTTGCGAAAAAGACAATT 341

Qy 61 ACAGTACCAAGGGGAAAGACTGTACTCTGAGGTTGGGAGATTGGATATCGAATCCCAG 120
Db 342 ACAGTACCAAGGGGAAAGACTGTACTCTGAGGTTGGGAGATTGGATATCGAATCCCAG 401

Qy 121 ACCTGTGCTTCTGACTACTCTTCTCTTCCACAGGCTCTTCAGATCAATATGGTCCATACTGT 180
Db 402 ACCTGTGCTTCTGACTACTCTTCTTCCACAGGCTCTTCAGATCAATATGGTCCATACTGT 461

Qy 181 GGAAGTATGACTGTTTCCAAAGAACTCTTGTTGAAACAAGTGAAGTAAACCGTCCCGCTTT 240
Db 462 GGAAGTATGACTGTTTCCAAAGAACTCTTGTTGAAACAAGTGAAGTAAACCGTCCCGCTTT 521

Qy 241 GAGAGTGGATCCCACTTTCTGCGCGGGGTTTTTCTGCTGACCTATCGGAGCAGCGACCAT 300
Db 522 GAGAGTGGATCCCACTTTCTGCGCGGGGTTTTTCTGCTGACCTATCGGAGCAGCGACCAT 581

Qy 301 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA 360
Db 582 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA 641

Qy 361 TTCTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 420
Db 642 TTCTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 701

Qy 421 TATAGATATACCTCTTTATTTGTCAAAGTCGCCATCCATGTCAGGAATATTCCTGATGAA 480
Db 702 TATAGATATACCTCTTTATTTGTCNAAGTCGCCATCCATGTCAGGAATATTCCTGATGAA 761

Qy 481 CTAGTGGCCAGATCAGTGTGCTTTCAAGCGAAAGGATCAGTGCATATGAAGGATTCGTCG 540
Db 762 CTAGTGGCCAGATCAGTGTGCTTTCAAGCGAAAGGATCAGTGCATATGAAGGATTCGTCG 821

Qy 541 GCCAATGGTGTCTTTTCGAGGGATGGTTCCCTGTCAGACAAGCGATTTCTGTGTTTACCTCC 600
Db 822 GCCAATGGTGTCTTTTCGAGGGATGGTTCCCTGTCAGACAAGCGATTTCTGTGTTTACCTCC 881

Qy 601 AATGGTTGACGACGATCCTTTGAGTTTGAACCTGACGGGCAATTCAGAGCTTCTTCTCTCA 660
Db 882 AATGGTTGACGACGATCCTTTGAGTTTGAACCTGACGGGCAATTCAGAGCTTCTTCTCTCA 941

Qy 661 TGGCAGTTCGGTCAATGAGAGTGGAGACCAAGTTTCACTTGGTCTCTGSCCAAGCCGACTT 720
Db 942 TGGCAGTTCGGTCAATGAGAGTGGAGACCAAGTTTCACTTGGTCTCTGSCCAAGCCGACTT 1001

Qy 721 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACAAACACACACAGAG 780

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Db 1002 CAGGACCAAGCCCATCATGGCTTCGGGCGACAGTAGCAACCAACCAACACGAGAG 1061
Qy 781 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATACAGGAATTAGGACCAAGATCT 840
Db 1062 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATACAGGAATTAGGACCAAGATCT 1121
Qy 841 ACACAGTCGAATCTCAACTTTTATGTTAAGAGTTTGTGATGAATCTCAAAAAACAATAAT 900
Db 1122 ACACAGTCGAATCTCAACTTTTATGTTAAGAGTTTGTGATGAATCTCAAAAAACAATAAT 1181
Qy 901 TCTAAGTGGAGACCTATAAAGGAATTGTGAATAATGAAGAAAAGTGTTCAGGGTAAC 960
Db 1182 TCTAAGTGGAGACCTATAAAGGAATTGTGAATAATGAAGAAAAGTGTTCAGGGTAAC 1241
Qy 961 TCTAACTTTTCGGGACCCAGTGCAAAACAAATTTTCATCCCTCCCATCGTGGCCAGATATGT 1020
Db 1242 TCTAACTTTTCGGGACCCAGTGCAAAACAAATTTTCATCCCTCCCATCGTGGCCAGATATGT 1301
Qy 1021 CGGGTTGTCCCCAGACATGGCCACAGAGGATAGCCTTTGAAGGTGGAGCTCATTTGGTTGC 1080
Db 1302 CGGGTTGTCCCCAGACATGGCCACAGAGGATAGCCTTTGAAGGTGGAGCTCATTTGGTTGC 1361
Qy 1081 CAGATTACAAAGGTAATGATTCATTTGGTGTGGGCGAAGACAAGTCAAAGCAACAGTGT 1140
Db 1362 CAGATTACAAAGGTAATGATTCATTTGGTGTGGGCGAAGACAAGTCAAAGCAACAGTGT 1421
Qy 1141 TCAACTAAGAAAAGAGATGAGACAATCAACAGGCCCATCCCTCGGAAGAAAACATCCACA 1200
Db 1422 TCAACTAAGAAAAGAGATGAGACAATCAACAGGCCCATCCCTCGGAAGAAAACATCCACA 1481
Qy 1201 GGAATAAACATTACAAAGGTGGCTATTCCATTTGGTGTCTCTTGTGTCTGGTGTGGCT 1260
Db 1482 GGAATAAACATTACAAAGGTGGCTATTCCATTTGGTGTCTCTTGTGTCTGGTGTGGCT 1541
Qy 1261 GGAATGGGATCTTTGAGGCTTTAGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Db 1542 GGAATGGGATCTTTGAGGCTTTAGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1601
Qy 1321 GCGAGGCTCAGAAAACAGACTGTGTGAAGCAGAGATTAATATCCCTTTGCCAGACATCAG 1380
Db 1602 GCGAGGCTCAGAAAACAGACTGTGTGAAGCAGAGATTAATATCCCTTTGCCAGACATCAG 1661
Qy 1381 TCAGCTGAGTTTACCATCAGCTATGATAATGAGAGAGAGATGACACAAAAAGTTAGATCTC 1440
Db 1662 TCAGCTGAGTTTACCATCAGCTATGATAATGAGAGAGAGATGACACAAAAAGTTAGATCTC 1721
Qy 1441 ATCAAGTATGATGGCAGGTAA 1464
Db 1722 ATCAAGTATGATGGCAGGTAA 1745
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RESULT 8

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US-10-783-528-24
; Sequence 24, Application US/10783528
; Publication No. US20040219579A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataasha
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
; FILE REFERENCE: 05882.0191.NPUS01
; CURRENT APPLICATION NUMBER: US/10/783.528
; CURRENT FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patent version 3.2
; SEQ ID NO 24
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-783-528-24
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Query Match 99.9%; Score 1462.4; DB 8; Length 2010;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTTCGGAAGACAAAT 60
Db 282 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTTCGGAAGACAAAT 341
Qy 61 ACAGTACCAAGGGGAAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCAG 120
Db 342 ACAGTACCAAGGGGAAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCAG 401
Qy 121 ACCTGTGCTTTCGACTATCTTCTTTCACAGCTCTTTCAGATCAATATGGTCCATCTGT 180
Db 402 ACCTGTGCTTTCGACTATCTTCTTTCACAGCTCTTTCAGATCAATATGGTCCATCTGT 461
Qy 181 GGAAGTATGACTGTTTCCCAAGAACTCTTGTGTGAACACAAAGTGAAGTAAACCGTCCGCTTT 240
Db 462 GGAAGTATGACTGTTTCCCAAGAACTCTTGTGTGAACACAAAGTGAAGTAAACCGTCCGCTTT 521
Qy 241 GAGAGTGGATCCCAATTTCTTGGCCGGGGTTTTTCTGCACTATCGAGCAGCAGCAT 300
Db 522 GAGAGTGGATCCCAATTTCTTGGCCGGGGTTTTTCTGCACTATCGAGCAGCAGCAT 581
Qy 301 CGAGATTTAATACATGTTTGGAAACGAGCTAGCCATTTTGAAGACAGAAATACAGCAA 360
Db 582 CGAGATTTAATACATGTTTGGAAACGAGCTAGCCATTTTGAAGACAGAAATACAGCAA 641
Qy 361 TTCTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 420
Db 642 TTCTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 701
Qy 421 TATAGAGATACCTCTTTTATTTGTGCAAGCTGCCATCCATGACAGAAATATTTGCTGATGAA 480
Db 702 TATAGAGATACCTCTTTTATTTGTGCAAGCTGCCATCCATGACAGAAATATTTGCTGATGAA 761
Qy 481 CTAGGTGGCCAGATCAGTGTGCTTTCAGCCGAAAGGATCAGTCGATATGAAGGATCTCG 540
Db 762 CTAGGTGGCCAGATCAGTGTGCTTTCAGCCGAAAGGATCAGTCGATATGAAGGATCTCG 821
Qy 541 GCCAATGGTCTTCTTTCGAGGGATGGTTCCCTCTCAGACAAAGCATTTCTGTTTACCTCC 600
Db 822 GCCAATGGTCTTCTTTCGAGGGATGGTTCCCTCTCAGACAAAGCATTTCTGTTTACCTCC 881
Qy 601 AATGGTTCAGCAGATCTTTGATTTTGAACCTTGAAGGCAAAATCAGAGCTTCTTCTCTCA 660
Db 882 AATGGTTCAGCAGATCTTTGATTTTGAACCTTGAAGGCAAAATCAGAGCTTCTTCTCTCA 941
Qy 661 TGGCAGTCCGTCATGAGAGTGGAGCCCAAGTTTCACTGTTCTCTGCGCCAGCCGACTT 720
Db 942 TGGCAGTCCGTCATGAGAGTGGAGCCCAAGTTTCACTGTTCTCTGCGCCAGCCGACTT 1001
Qy 721 CAGGACCAAGGCCCATCATGGGCTTTCGGGCGACAGTAGCAACCAACCAACCAACGAGAG 780
Db 1002 CAGGACCAAGGCCCATCATGGGCTTTCGGGCGACAGTAGCAACCAACCAACGAGAG 1061
Qy 781 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATTAACAGGAATTAGGACCAAGATCT 840
Db 1062 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATTAACAGGAATTAGGACCAAGATCT 1121
Qy 841 ACACAGTCGAATCTCAACTTTTATGTTAAGAGTTTGTGATGAATCTCAAAAAACAATAAT 900
Db 1122 ACACAGTCGAATCTCAACTTTTATGTTAAGAGTTTGTGATGAATCTCAAAAAACAATAAT 1181
Qy 901 TCTAAGTGGAGACCTATAAAGGAATTGTGAATAATGAAGAAAAGTGTTCAGGGTAAC 960
Db 1182 TCTAAGTGGAGACCTATAAAGGAATTGTGAATAATGAAGAAAAGTGTTCAGGGTAAC 1241
Qy 961 TCTAACTTTTCGGGACCCAGTGCAAAACAAATTTTCATCCCTCCCATCGTGGCCAGATATGT 1020
Db 1242 TCTAACTTTTCGGGACCCAGTGCAAAACAAATTTTCATCCCTCCCATCGTGGCCAGATATGT 1301
Qy 1021 CGGGTTGTCCCCAGACATGGCCACAGAGGATAGCCTTTGAAGGTGGAGCTCATTTGGTTGC 1080
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Db 1302 CGGGTTGTCCTCCAGCATGGCCAGAGGATAGCCTTGAAGTGGAGCTCATTTGGTTC 1361
Qy 1081 CAGATTACCAAGTATGATTCATTTGGTGGGCGAAGTCAAGTCAAGCAGTGT 1140
Db 1362 CAGATTACCAAGTATGATTCATTTGGTGGGCGAAGTCAAGTCAAGCAGTGT 1421
Qy 1141 TCAACTAAGAAAGATGAGACAATCAACAAGGCCCATCCCTCGGAAGAAACATCCACA 1200
Db 1422 TCAACTAAGAAAGATGAGACAATCAACAAGGCCCATCCCTCGGAAGAAACATCCACA 1481
Qy 1201 GGAATAAACATTAACAGGTGGCTATTCATTTGGTGGTCTCTTTGGTGGTGGTGGT 1260
Db 1482 GGAATAAACATTAACAGGTGGCTATTCATTTGGTGGTCTCTTTGGTGGTGGTGGT 1541
Qy 1261 GGAATCGGGATCTTTGAGAGCTTTTGAAGAAGAAAGAAAGTCCGTATGGATCA 1320
Db 1542 GGAATCGGGATCTTTGAGAGCTTTTGAAGAAGAAAGAAAGTCCGTATGGATCA 1601
Qy 1321 GCGAGGCTCAGAAACAGACTGTTGGAAGCAGATTAAATATATCCCTTTGCCAGACATCAG 1380
Db 1602 GCGAGGCTCAGAAACAGACTGTTGGAAGCAGATTAAATATATCCCTTTGCCAGACATCAG 1661
Qy 1381 TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAAGAGATGACACAAAGTTAGATCTC 1440
Db 1662 TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAAGAGATGACACAAAGTTAGATCTC 1721
Qy 1441 ATCACAAGTGATGCGAGTTAA 1464
Db 1722 ATCACAAGTGATGCGAGTTAA 1745

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RESULT 9

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US-09-759-1308-72
; Sequence 72, Application US/097591308
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D.
; APPLICANT: Barnes, Thomas S
; APPLICANT: KIRST, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE OF INVENTION: USES.
; FILE REFERENCE: MPI00-5350NM
; CURRENT APPLICATION NUMBER: US/09/759,1308
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23

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; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-1308-72

Query Match 99.7%; Score 1459.8; DB 3; Length 2145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTCTTTTGGGAAAAGACAATT 60
Db 157 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTCTTTTGGGAAAAGACAATT 216
Qy 61 ACAGTACCAAAAGGGGAAAAGACTGATTTCTGAGGTGGGAGATTGGATATCGAATCCCAG 120
Db 217 ACAGTACCAAAAGGGGAAAAGACTGATTTCTGAGGTGGGAGATTGGATATCGAATCCCAG 276
Qy 121 ACCTGTGCTTCTGACTATCTTCTTCCAGAGCTCTTCAGATCAATATGTCATCTGT 180
Db 277 ACCTGTGCTTCTGACTATCTTCTTCCAGAGCTCTTCAGATCAATATGTCATCTGT 336
Qy 181 GGAAGTATCAGCTGTTCCCAAGAACTCTTTGTTGAACACAGTGAAGTAAACCGTCCGCTTT 240
Db 337 GGAAGTATCAGCTGTTCCCAAGAACTCTTTGTTGAACACAGTGAAGTAAACCGTCCGCTTT 396
Qy 241 GAGATGGATCCCACATTTCTGCGCGGGGTTTTTCTGCTACCTATGCGAGCAGCGACCAT 300
Db 397 GAGATGGATCCCACATTTCTGCGCGGGGTTTTTCTGCTACCTATGCGAGCAGCGACCAT 456
Qy 301 CCAGATTTAATAACATGTTTGGAAACAGCTAGCCATTTTGAAGACAGAAATACAGCAAA 360
Db 457 CCAGATTTAATAACATGTTTGGAAACAGCTAGCCATTTTGAAGACAGAAATACAGCAAA 516
Qy 361 TTCTGCCAGCTGGTTGTAGACAGCTAGCAGAGACATTTCTGGGAAATATGGTAGATGA 420
Db 517 TTCTGCCAGCTGGTTGTAGACAGCTAGCAGAGACATTTCTGGGAAATATGGTAGATGA 576
Qy 421 TATAGAGATACCTCTTTTATTTGTCAAAGCTGCCATCCATCGAGGAAATAATTTGCTGATGA 480
Db 577 TATAGAGATACCTCTTTTATTTGTCAAAGCTGCCATCCATCGAGGAAATAATTTGCTGATGA 636
Qy 481 CTAGTGGCCAGATCAGTGTCTTCAGCGCAAGGGATCAGTCGATATGAAGGATCTG 540
Db 637 CTAGTGGCCAGATCAGTGTCTTCAGCGCAAGGGATCAGTCGATATGAAGGATCTG 696
Qy 541 GCCAATGGTGTCTTTTCGAGGGATGTTTCCCTGTGTCAGACAGAGATTTCTGTTTACCTCC 600
Db 697 GCCAATGGTGTCTTTTCGAGGGATGTTTCCCTGTGTCAGACAGAGATTTCTGTTTACCTCC 756
Qy 601 AATGGTTGAGCAGATCTTTGAGTTTGAACCTGAGCGGCAAAATCAGAGCTTTCTCTCA 660
Db 757 AATGGTTGAGCAGATCTTTGAGTTTGAACCTGAGCGGCAAAATCAGAGCTTTCTCTCA 816
Qy 661 TGGCAGTGGTCAATGAGAGTGGAGACCAAGTTCTACTGTCTCTGCGCAAGCCGACTT 720
Db 817 TGGCAGTGGTCAATGAGAGTGGAGACCAAGTTCTACTGTCTCTGCGCAAGCCGACTT 876
Qy 721 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACAACCAACCAAGCAGAG 780
Db 877 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACAACCAACCAAGCAGAG 936
Qy 781 TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAAAATACAGGAAATTAGGACCACAGGATCT 840
Db 937 TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAAAATACAGGAAATTAGGACCACAGGATCT 996
Qy 841 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAACTTTCAAAAACAATAAT 900
Db 997 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAACTTTCAAAAACAATAAT 1056

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QY 901 TCTAAGTGGAGACCTATAAGGAATGTGAATAAGAAAAGGTGTTTCAGGGTAAC 960
Db 1057 TCTAAGTGGAGACCTATAAGGAATGTGAATAAGAAAAGGTGTTTCAGGGTAAC 1116
QY 961 TCTAAGTGGAGACCTATAAGGAATGTGAATAAGAAAAGGTGTTTCAGGGTAAC 1020
Db 1117 TCTAAGTGGAGACCTATAAGGAATGTGAATAAGAAAAGGTGTTTCAGGGTAAC 1176
QY 1021 CGGGTGTGCCCCAGACATGCGCAGAGATAGCCTTGAAGGTGGAGCTCATTTGGTTGC 1080
Db 1177 CGGGTGTGCCCCAGACATGCGCAGAGATAGCCTTGAAGGTGGAGCTCATTTGGTTGC 1236
QY 1081 CAGATTACACAGGTAAATGATTCATTGTTGGTGGCGCAAGACAAGTCAAAGCACCAGTGT 1140
Db 1237 CAGATTACACAGGTAAATGATTCATTGTTGGTGGCGCAAGACAAGTCAAAGCACCAGTGT 1296
QY 1141 TCAACTAAGAAAAGAGTGAAGATCAACAAGGCCCATCCCTCGGAGAAACATCCACA 1200
Db 1297 TCAACTAAGAAAAGAGTGAAGATCAACAAGGCCCATCCCTCGGAGAAACATCCACA 1356
QY 1201 GGAATAAACATTACAAGCGTGGCTATTCCATTGGTGTCTCTGTTGCTGGTGTGTTGCT 1260
Db 1357 GGAATAAACATTACAAGCGTGGCTATTCCATTGGTGTCTCTGTTGCTGGTGTGTTGCT 1416
QY 1261 GGAATGGGGATCTTTGACGCTTTAGAAAAGAAAGAAAGAAAGTCCGTATGGATCA 1320
Db 1417 GGAATGGGGATCTTTGACGCTTTAGAAAAGAAAGAAAGAAAGTCCGTATGGATCA 1476
QY 1321 GCGAGGCTCAGAAAACAGACTGTTGAAGCAGATTAATATCCCTTGGCAGACATCAG 1380
Db 1477 GCGAGGCTCAGAAAACAGACTGTTGAAGCAGATTAATATCCCTTGGCAGACATCAG 1536
QY 1381 TCAGCTCAGTTTACCATCAGCTATGATAATGAGAGGAGATGACACAAAAAGTTAGATCTC 1440
Db 1537 TCAGCTCAGTTTACCATCAGCTATGATAATGAGAGGAGATGACACAAAAAGTTAGATCTC 1596
QY 1441 ATCAAAAGTGATGGCAGGTTA 1463
Db 1597 ATCAAAAGTGATGGCAGGTTA 1619
RESULT 10
US-10-741-790-72
; Sequence 72, Application US/10741790
; Publication No. US20040121396A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-5350MIM
; CURRENT APPLICATION NUMBER: US/10741790
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
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; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-790-72
Query Match 99.7%; Score 1459.8; DB 7; Length 2145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGACATCTAAGAAATTTATCCGGGACCTACCCCAATCACACTGTTTTCGGAAGACAAAT 60
Db 157 ATGACATCTAAGAAATTTATCCGGGACCTACCCCAATCACACTGTTTTCGGAAGACAAAT 216
QY 61 ACAGTACCAAGGGGAAAGACTGATCTGAGGTGGGAGATTTGGATATCGAATCCAG 120
Db 217 ACAGTACCAAGGGGAAAGACTGATCTGAGGTGGGAGATTTGGATATCGAATCCAG 276
QY 121 ACCTGTGCTTCACTATCTTCTTCAACAGCTTTCAGATCAATATGTCCTCACTGT 180
Db 277 ACCTGTGCTTCACTATCTTCTTCAACAGCTTTCAGATCAATATGTCCTCACTGT 336
QY 181 GGAAGTATGACTGTTCCCAAGAACTCTGTTGAAACACAGTCAAGTAAACCGTCGCTTT 240
Db 337 GGAAGTATGACTGTTCCCAAGAACTCTGTTGAAACACAGTCAAGTAAACCGTCGCTTT 396
QY 241 GAGAGTGGATCCACATTTCTGCGCGGGTCTTGTGACCTATCGAGCAGCAGCAT 300
Db 397 GAGAGTGGATCCACATTTCTGCGCGGGTCTTGTGACCTATCGAGCAGCAGCAT 456
QY 301 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACAGAAA 360
Db 457 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACAGAAA 516
QY 361 TTCTGCCAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 420
Db 517 TTCTGCCAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 576
QY 421 TATAGAGATACCTCTTTTATTTGTCAGAACTGCCATCCATCAGGAATAATTTGCTGATGAA 480
Db 577 TATAGAGATACCTCTTTTATTTGTCAGAACTGCCATCCATCAGGAATAATTTGCTGATGAA 636
QY 481 CTAGGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGATCAGTCGATATGAAGGATTCGT 540
Db 637 CTAGGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGATCAGTCGATATGAAGGATTCGT 696
QY 541 GCCAATGGTCTTTCTTTCGAGGGATGGTTCCCTCTGACAGCAAGGATTTCTGTTTACCTCC 600
Db 697 GCCAATGGTCTTTCTTTCGAGGGATGGTTCCCTCTGACAGCAAGGATTTCTGTTTACCTCC 756
QY 601 AATGTTTGCAGCAGATCCTTTGAGTTTTTGAACCTGACCGGCAAAATCAGAGCTTCTTCTCA 660
Db 757 AATGTTTGCAGCAGATCCTTTGAGTTTTTGAACCTGACCGGCAAAATCAGAGCTTCTTCTCA 816
QY 661 TGGCAGTCCGTCAATGAGAGTGGAGACCAAGTTCACGTCTCTGCTCCCAAGCCGACTT 720
Db 817 TGGCAGTCCGTCAATGAGAGTGGAGACCAAGTTCACGTCTCTGCTCCCAAGCCGACTT 876
QY 721 CAGGACCAAGGCCCATCATCGGCTTTCGGGCGACAGTAGCAACACCAACCAACGAGAG 780
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Db 877 CAGGACCAAGCCCATCATGGCTTCGGGCGACAGTAGCAACCAACCAACCAACAGGAG 936
Qy 781 TGCTGAGATCGATTGGGGGAGAAAAGAAATACAGGAATAGGACCAAGATCT 840
Db 937 TGCTGAGATCGATTGGGGGAGAAAAGAAATACAGGAATAGGACCAAGATCT 996
Qy 841 ACACAGTCGAACCTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAACAATAAT 900
Db 997 ACACAGTCGAACCTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAACAATAAT 1056
Qy 901 TCTAAGTCGAAGACCTATAAGGAATGTGAATTAAGAAAGAGTGTTCAGGGTAAC 960
Db 1057 TCTAAGTCGAAGACCTATAAGGAATGTGAATTAAGAAAGAGTGTTCAGGGTAAC 1116
Qy 961 TCTAAGTCGGGACCCAGTCAAAACAATTTCACTCCCTCCCATCGTGGCCAGATATG 1020
Db 1117 TCTAAGTCGGGACCCAGTCAAAACAATTTCACTCCCTCCCATCGTGGCCAGATATG 1176
Qy 1021 CGGGTTGTCCCCAGACATGGCACAGAGATAGCCCTTGAAGGTGGAGCTCATTTGGTTGC 1080
Db 1177 CGGGTTGTCCCCAGACATGGCACAGAGATAGCCCTTGAAGGTGGAGCTCATTTGGTTGC 1236
Qy 1081 CAGATTACACAAGGTATGATTCATTGGTGTGGCGCAAGACAAGTCAAAGCACAGTGT 1140
Db 1237 CAGATTACACAAGGTATGATTCATTGGTGTGGCGCAAGACAAGTCAAAGCACAGTGT 1296
Qy 1141 TCAACTAAGAAAGATGAGCAATCACAGGCCCATCCCTCGAAGAAACATCCACA 1200
Db 1297 TCAACTAAGAAAGATGAGCAATCACAGGCCCATCCCTCGAAGAAACATCCACA 1356
Qy 1201 GGAATAAACATTAACAAGGTGGCTATTCCATTGGTGTCTCTCTGTTGCTGGTGTGCT 1260
Db 1357 GGAATAAACATTAACAAGGTGGCTATTCCATTGGTGTCTCTCTGTTGCTGGTGTGCT 1416
Qy 1261 GGAATGGGATCTTTGAGCCTTTAGAAAGAAAGAAAGAAAGTCCGTATGATCA 1320
Db 1417 GGAATGGGATCTTTGAGCCTTTAGAAAGAAAGAAAGAAAGTCCGTATGATCA 1476
Qy 1321 GCGAGGCTCAGAAAACAGACTGTGGAAGCAGATTAAATATATCCCTTCCAGACATCAG 1380
Db 1477 GCGAGGCTCAGAAAACAGACTGTGGAAGCAGATTAAATATATCCCTTCCAGACATCAG 1536
Qy 1381 TCAGCTGAGTTTACCATCAGCTATGATATGAGAAGGAGATGACACAAAAGTTAGATCTC 1440
Db 1537 TCAGCTGAGTTTACCATCAGCTATGATATGAGAAGGAGATGACACAAAAGTTAGATCTC 1596
Qy 1441 ATCACAAGTGATGGCAGTTA 1463
Db 1597 ATCACAAGTGATGGCAGTTA 1619

RESULT 11

US-10-312-352-47

; Sequence 47, Application US/10312352

; Publication No. US20040053824A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom

; APPLICANT: YUE, Henry; AZIMZAI, Yalda

; APPLICANT: HE, Ann; BATRA, Sajeev

; APPLICANT: LO, Terence P.; NGUYEN, Dammiel B.

; APPLICANT: BURLILL, John D.; MARCUS, Gregory A.

; APPLICANT: ZINGLER, Kurt A.; GANDHI, Ameena R.

; APPLICANT: LAL, Preeti G.; KEARNEY, Liam

; APPLICANT: BURFORD, Neil; YAO, Monique G.

; APPLICANT: CHAWLA, Narinder K.; ELLIOT, Vicki S.

; APPLICANT: ARVIZU, Chandra S.; KHAN, Farrah A.

; APPLICANT: BAUGHN, Mariah R.; HAPALIA, April, J.A.

; APPLICANT: POLICKY, Jennifer L.; AU-YOUNG, Janice K.

; APPLICANT: LU, Yan; BOROWSKY, Mark L.

; APPLICANT: LU, Dzung Aina M.; RAMKUMAR, Jayalaxmi

; APPLICANT: YANG, Junming; GURURAJAN, Rajagopal

; APPLICANT: WARREN, Bridget A.; GIETZEN, Kimberly J.

; APPLICANT: XU, Yuming; KALLICK, Deborah A.
; APPLICANT: LEE, Ernestine A.; THANGAVELU, Kavitha
; APPLICANT: DELEANE, Angelo M.; LEE, Sally
; TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
; FILE REFERENCE: PP-0794 USN
; CURRENT APPLICATION NUMBER: US/10/312,352
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: PCT/US01/21067
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,454
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/219,462
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 60/240,111
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: US 60/240,106
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: US 60/244,021
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/248,887
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/249,570
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PERL Program
; SEQ ID NO 47
; LENGTH: 2888
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040053824A1 184661CB1
US-10-312-352-47

Query Match 99.7%; Score 1459.8; DB 7; Length 2888;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTGGGAAAGACAATT 60
Db 282 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTGGGAAAGACAATT 341
Qy 61 ACAGTACCAAGGGGAAAAGAGCTGATTCTGAGGTGGGAGATTGGATATCGAATCCAG 120
Db 342 ACAGTACCAAGGGGAAAAGAGCTGATTCTGAGGTGGGAGATTGGATATCGAATCCAG 401
Qy 121 ACTGTGCTTTCGACTATCTCTCTTCCAGCTCTTTCAGATCAATATGGTCCATCTGT 180
Db 402 ACTGTGCTTTCGACTATCTCTCTTCCAGCTCTTTCAGATCAATATGGTCCATCTGT 461
Qy 181 GGAAGTATGACTGTTCCCAAGAACTCTTGTGAAACACAAGTGAAGTAAACCGTCCGCTTT 240
Db 462 GGAAGTATGACTGTTCCCAAGAACTCTTGTGAAACACAAGTGAAGTAAACCGTCCGCTTT 521
Qy 241 GAGAGTGAATCCCAATTTCTGCGCGGGGTTTTTGTGACCTATCGGAGCAGCGACCAT 300
Db 522 GAGAGTGAATCCCAATTTCTGCGCGGGGTTTTTGTGACCTATCGGAGCAGCGACCAT 581
Qy 301 CCAGATTTAATAACATGTTTGGAAAGAGCTAGCCATTATTGGAAGACAGATAACAGAAA 360
Db 582 CCAGATTTAATAACATGTTTGGAAAGAGCTAGCCATTATTGGAAGACAGATAACAGAAA 641
Qy 361 TTCTGCCAGCTGTTGTAGACAGCTAGCAGGAGACATTTCTGGGAAATATGGTAGATGA 420
Db 642 TTCTGCCAGCTGTTGTAGACAGCTAGCAGGAGACATTTCTGGGAAATATGGTAGATGA 701
Qy 421 TATAGATATACCTCTTTTATTGTGCAAGCTGCCATCCATCGACGAATAATTGCTGATGAA 480
Db 702 TATAGATATACCTCTTTTATTGTGCAAGCTGCCATCCATCGACGAATAATTGCTGATGAA 761
Qy 481 CTAGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGATCAGTCGATATGAAGGATTTCTG 540
Db 762 CTAGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGATCAGTCGATATGAAGGATTTCTG 821


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QY 541 GCCAATGGTGTCTTTTCGAGGATGGTTCCTGTGACAGCAAGCATTTCTGTTCACCTCC 600
Db 822 GCCAATGGTGTCTTTTCGAGGATGGTTCCTGTGACAGCAAGCATTTCTGTTCACCTCC 881
QY 601 AATGGTTGACGACAGATCCTTTGAGTTTGAACCTTGACGGGCAATTCAGAGCTTCTTCTCA 660
Db 882 AATGGTTGACGACAGATCCTTTGAGTTTGAACCTTGACGGGCAATTCAGAGCTTCTTCTCA 941
QY 661 TGGCAGTCGGTCAATGAGAGTGAGACCAAGTTTCACTGGTCTCTCGCCCAAGCCGACATT 720
Db 942 TGGCAGTCGGTCAATGAGAGTGAGACCAAGTTTCACTGGTCTCTCGCCCAAGCCGACATT 1001
QY 721 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACCAACCAACCAACGAGAG 780
Db 1002 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACCAACCAACCAACGAGAG 1061
QY 781 TGGCTGGAGATCGAATTTGGGGGAGAAAGAAATTAACAGGAATTAGGACCAAGATCT 840
Db 1062 TGGCTGGAGATCGAATTTGGGGGAGAAAGAAATTAACAGGAATTAGGACCAAGATCT 1121
QY 841 ACACAGTCGAACTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAACAATAAT 900
Db 1122 ACACAGTCGAACTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAACAATAAT 1181
QY 901 TCTAAGTGAAGACCTATAAAGCAATTTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 960
Db 1182 TCTAAGTGAAGACCTATAAAGCAATTTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1241
QY 961 TCTAAGTTCGGGACCCAGTGCAAAACAAATTTCACTCCCTCCCATCGTGGCCAGATATGT 1020
Db 1242 TCTAAGTTCGGGACCCAGTGCAAAACAAATTTCACTCCCTCCCATCGTGGCCAGATATGT 1301
QY 1021 CGGGTGTCCCCAGACATGGCACGAGATAGCTTTGAAGTGGAGCTCATTTGGTTC 1080
Db 1302 CGGGTGTCCCCAGACATGGCACGAGATAGCTTTGAAGTGGAGCTCATTTGGTTC 1361
QY 1081 CAGATTACAAAGTAATGATTCATTGGTGTGGCGCAAGCAAGTCAAAAGCACCAGTGT 1140
Db 1362 CAGATTACAAAGTAATGATTCATTGGTGTGGCGCAAGCAAGTCAAAAGCACCAGTGT 1421
QY 1141 TCAACTAAGAAAGAAAGATGAGACAATCAAGGCCCATTCCTCGGAAGAAACATCCACA 1200
Db 1422 TCAACTAAGAAAGAAAGATGAGACAATCAAGGCCCATTCCTCGGAAGAAACATCCACA 1481
QY 1201 GGAATAAACATTACAAAGGTGGCTATTTCATTGGTGTCTCTTGTGCTGGTGTGCT 1260
Db 1482 GGAATAAACATTACAAAGGTGGCTATTTCATTGGTGTCTCTTGTGCTGGTGTGCT 1541
QY 1261 GGAATGGGGATCTTTTGCAGCCTTTAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1320
Db 1542 GGAATGGGGATCTTTTGCAGCCTTTAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1601
QY 1321 GCGAGGCTCAGAAAACAGACTGTGTGAAGCAGATTAAATATCCCTTTGCCAGACATCAG 1380
Db 1602 GCGAGGCTCAGAAAACAGACTGTGTGAAGCAGATTAAATATCCCTTTGCCAGACATCAG 1661
QY 1381 TCAGTCAGTTTACCATCAGCTATGTAATGAGAGGAGATGACACAAAAGTTAGATCTC 1440
Db 1662 TCAGTCAGTTTACCATCAGCTATGTAATGAGAGGAGATGACACAAAAGTTAGATCTC 1721
QY 1441 ATCAAAAGTGATATGGCAGGTTA 1463
Db 1722 ATCAAAAGTGATATGGCAGGTTA 1744
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RESULT 12

US-10-003-132-1

; Sequence 1, Application US/10003132

; Publication No. US20020192750A1

; GENERAL INFORMATION:

; APPLICANT: Fox, Brian A.

; APPLICANT: Geo, Zeren

```
; APPLICANT: Shoemaker, Kimberly E.
; TITLE OF INVENTION: NEUROFILIN HOMOLOG 2CUB5
; FILE REFERENCE: 00-62
; CURRENT APPLICATION NUMBER: US/10/003,132
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/249,004
; PRIOR FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (76)...(2223)
US-10-003-132-1
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Query Match 99.7%; Score 1459.8; DB 5; Length 3151;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTTCGAAAAAGACAATT 60
Db 232 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTTCGAAAAAGACAATT 291
QY 61 ACAGTACCAAAAGGGGAAAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCCAG 120
Db 292 ACAGTACCAAAAGGGGAAAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCCAG 351
QY 121 ACCTGTGCTTCTGACTATCTTTCTTTTCAACAGCTCTTCAGATCAATATGTCATCTGT 180
Db 352 ACCTGTGCTTCTGACTATCTTTCTTTTCAACAGCTCTTCAGATCAATATGTCATCTGT 411
QY 181 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTTCAACAGTCAAGTAAACCGTCCGCTTT 240
Db 412 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTTCAACAGTCAAGTAAACCGTCCGCTTT 471
QY 241 GAGAGTGGATCCCAACATTTCTGGCCGGGGTTTTTGTGCTGACCTATGCGAGCAGCACCAT 300
Db 472 GAGAGTGGATCCCAACATTTCTGGCCGGGGTTTTTGTGCTGACCTATGCGAGCAGCACCAT 531
QY 301 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA 360
Db 532 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA 591
QY 361 TTCTGCCACGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGTTAGATGGA 420
Db 592 TTCTGCCACGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGTTAGATGGA 651
QY 421 TATAGAGATACCTCTTTTATTTGTCAAAGCTGCCATCCATCCATGAGGAATATTTGCTGATGA 480
Db 652 TATAGAGATACCTCTTTTATTTGTCAAAGCTGCCATCCATCCATGAGGAATATTTGCTGATGA 711
QY 481 CTAGTGGCCAGATCAGTGTCTTCAGGCAAGGGATCAGTCGATATGAGGGATCTG 540
Db 712 CTAGTGGCCAGATCAGTGTCTTCAGGCAAGGGATCAGTCGATATGAGGGATCTG 771
QY 541 GCCAATGGTGTCTTTTCGAGGATGGTTCCTGTGACAGCAAGCATTTCTGTTTACCTCC 600
Db 772 GCCAATGGTGTCTTTTCGAGGATGGTTCCTGTGACAGCAAGCATTTCTGTTTACCTCC 831
QY 601 AATGGTTGACGACAGATCCTTTGAGTTTGAACCTTGACCGGCAATTCAGAGCTTCTTCTCA 660
Db 832 AATGGTTGACGACAGATCCTTTGAGTTTGAACCTTGACCGGCAATTCAGAGCTTCTTCTCA 891
QY 661 TGGCAGTCGGTCAATGAGAGTGAGACCAAGTTTCACTGGTCTCTCGCCCAAGCCGACATT 720
Db 892 TGGCAGTCGGTCAATGAGAGTGAGACCAAGTTTCACTGGTCTCTCGCCCAAGCCGACATT 951
QY 721 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACCAACCAACCAACGAGAG 780
Db 952 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACCAACCAACCAACGAGAG 1011
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Db      828 AATGGTTGACGAGATCCTTGAAGTTTGAACCTGACGGGCAATCAGAGCTTCTCTCA 887
Qy      661 TGGCAGTCGGTCAATCAGAGTGAGACCAAGTTCACTGGTCTCCTCGCCAAAGCCGACTT 720
Db      888 TGGCAGTCGGTCAATCAGAGTGAGACCAAGTTCACTGGTCTCCTCGCCAAAGCCGACTT 947
Qy      721 CAGGACCAAGGCCCATCATCGGGCTTCGGGCGACAGTAGCAACAACCAACCAACGAGAG 780
Db      948 CAGGACCAAGGCCCATCATCGGGCTTCGGGCGACAGTAGCAACAACCAACCAACGAGAG 1007
Qy      781 TGCGCTGGAGATCGAATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAAGATCT 840
Db      1008 TGCGCTGGAGATCGAATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAAGATCT 1067
Qy      841 ACACAGTCGAATCTCAACTTTATGTTAAAGGATTTGTGATGAATCTTCAAAAACAATAAT 900
Db      1068 ACACAGTCGAATCTCAACTTTATGTTAAAGGATTTGTGATGAATCTTCAAAAACAATAAT 1127
Qy      901 TCTAAGTGAAGACCTATAAAGGAATTTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 960
Db      1128 TCTAAGTGAAGACCTATAAAGGAATTTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1187
Qy      961 TCTAAGTGAAGACCTATAAAGGAATTTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1020
Db      1188 TCTAAGTGAAGACCTATAAAGGAATTTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1247
Qy      1021 CGGGTTGTCGCCCGACATCGCCACGAGATAGCCTTGAAGGTGGAGCTCAATGGTTGC 1080
Db      1248 CGGGTTGTCGCCCGACATCGCCACGAGATAGCCTTGAAGGTGGAGCTCAATGGTTGC 1307
Qy      1081 CAGATTACACAAGTGAATGATTTCAATCGGTGTGGCGCAAGACAAGTCAAAGCACCAGTGT 1140
Db      1308 CAGATTACACAAGTGAATGATTTCAATCGGTGTGGCGCAAGACAAGTCAAAGCACCAGTGT 1367
Qy      1141 TCAACTAAGAAAGAGATGAGACAATCAACAAGGCCCATTCCTCGGAAGAAAACATCCACA 1200
Db      1368 TCAACTAAGAAAGAGATGAGACAATCAACAAGGCCCATTCCTCGGAAGAAAACATCCACA 1427
Qy      1201 GGAATAAACAATTACAAGGTGGCTATTCCTATGGTGTCTCTTGTCTCTGGTGTGCT 1260
Db      1428 GGAATAAACAATTACAAGGTGGCTATTCCTATGGTGTCTCTTGTCTCTGGTGTGCT 1487
Qy      1261 GGAATGGGGATCTTTGCGAGCCTTTAGAAAAGAAAGAAAGAAAGTCCGTATGGATCA 1320
Db      1488 GGAATGGGGATCTTTGCGAGCCTTTAGAAAAGAAAGAAAGAAAGTCCGTATGGATCA 1547
Qy      1321 GCGAGAGCTCAGAAAACAGACTGTGGAGCAGATTTAAATATCCCTTTGCCAGACATCAG 1380
Db      1548 GCGAGAGCTCAGAAAACAGACTGTGGAGCAGATTTAAATATCCCTTTGCCAGACATCAG 1607
Qy      1381 TCAGCTGAGTTTACCATCAGCTATGATTAATCAGAGGAGATGACACAAAAGTTAGATCTC 1440
Db      1608 TCAGCTGAGTTTACCATCAGCTATGATTAATCAGAGGAGATGACACAAAAGTTAGATCTC 1667
Qy      1441 ATCAAAAGTGAATGGCAGGTTA 1463
Db      1668 ATCAAAAGTGAATGGCAGATTA 1690
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RESULT 14

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US-10-741-790-71
; Sequence 71, Application US/10741790
; Publication No. US20040121396A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kiret, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
```

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; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/10741,790
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 3594
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-741-790-71
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Query Match 99.7%; Score 1459.8; DB 7; Length 3594;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ATGACATCTAAGAAATATATCCGGGACCTACCCCAATCACACTGTTTCGGAAGAACAAATT 60
Db      228 ATGACATCTAAGAAATATATCCGGGACCTACCCCAATCACACTGTTTCGGAAGAACAAATT 287
Qy      61 ACAGTACCAAGGGGAAAGACTGATTCAGAGTTGGGAGATTTGGATATCGAATCCAG 120
Db      288 ACAGTACCAAGGGGAAAGACTGATTCAGAGTTGGGAGATTTGGATATCGAATCCAG 347
Qy      121 ACCTGTGCTTCTGACTATCTTCTTCCACAGCTCTTTCAGATCAATATGGTCCATCTGT 180
Db      348 ACCTGTGCTTCTGACTATCTTCTTCCACAGCTCTTTCAGATCAATATGGTCCATCTGT 407
Qy      181 GGAAGTATGACTGTTCCTCAAGAACTCTTGTGGAACAAGTGAAGTAAACGTCGCTTT 240
Db      408 GGAAGTATGACTGTTCCTCAAGAACTCTTGTGGAACAAGTGAAGTAAACGTCGCTTT 467
Qy      241 GAGAGTGGATCCCAATTTCTGGCCGGGGTTTTTGTCTGCTACCTATGGAGCAGGACCAT 300
Db      468 GAGAGTGGATCCCAATTTCTGGCCGGGGTTTTTGTCTGCTACCTATGGAGCAGGACCAT 527
Qy      301 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACAGAAA 360
Db      528 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACAGAAA 587
Qy      361 TTCTGCCAGCTGGTCTGAGAGCTAGCAGGAGACATTTCTCGGAATATGTTAGATCGA 420
Db      588 TTCTGCCAGCTGGTCTGAGAGCTAGCAGGAGACATTTCTCGGAATATGTTAGATCGA 647
Qy      421 TATAGAGATACCTCTTTTATTTGTGCAAAAGCTGCCATCCATGCCAGGAATATTTCTGATGAA 480
Db      648 TATAGAGATACCTCTTTTATTTGTGCAAAAGCTGCCATCCATGCCAGGAATATTTCTGATGAA 707
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481 CTAGGTGGCCAGATCATGTGCTTTCAGCGCAAGGGATCAGTCGATATGAAGGATTCTG 540
708 CTAGGTGGCCAGATCATGTGCTTTCAGCGCAAGGGATCAGTCGATATGAAGGATTCTG 767
541 GCCAATGGTGTCTTTCGAGGATAGTTCCTGTGACAAAGGATTTCTGTTTACCTCC 600
768 GCCAATGGTGTCTTTCGAGGATAGTTCCTGTGACAAAGGATTTCTGTTTACCTCC 827
601 AATGGTTGCAGCAGATCTTGAAGTTTGAACCTTGCAGGCAAAATCAGAGCTTCTTCTCA 660
828 AATGGTTGCAGCAGATCTTGAAGTTTGAACCTTGCAGGCAAAATCAGAGCTTCTTCTCA 887
661 TGGCAGTCGTCATTAAGAGTGGAGACCAAGTTTCACTGGTCTCTTGGCCCAAGCCGACTT 720
888 TGGCAGTCGTCATTAAGAGTGGAGACCAAGTTTCACTGGTCTCTTGGCCCAAGCCGACTT 947
721 CAGGACCAAGGCCCATCATGGCTTTCGGGCGACAGTAGCAACCAACCAACCAACGAGAG 780
948 CAGGACCAAGGCCCATCATGGCTTTCGGGCGACAGTAGCAACCAACCAACCAACGAGAG 1007
781 TGGCTCGAGATCGATTTCGGGGGAGAAAAGAAAATACAGGAATTAGGACCAAGATCT 840
1008 TGGCTCGAGATCGATTTCGGGGGAGAAAAGAAAATACAGGAATTAGGACCAAGATCT 1067
841 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAATTTCAAAAACAATAAT 900
1068 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAATTTCAAAAACAATAAT 1127
901 TCTAAGTGGAGACCTTATAAGGAATTTGGAATTAAGAAAGAGTGTTCAGGGTAAC 960
1128 TCTAAGTGGAGACCTTATAAGGAATTTGGAATTAAGAAAGAGTGTTCAGGGTAAC 1187
961 TCTAAGTGGAGACCTTATAAGGAATTTGGAATTAAGAAAGAGTGTTCAGGGTAAC 1020
1188 TCTAAGTGGAGACCTTATAAGGAATTTGGAATTAAGAAAGAGTGTTCAGGGTAAC 1247
1021 CGGGTTGTCTCCCGCAGATGGCCACAGAGGATAGCTTGAAGGTGGAGCTCATTTGGTTGC 1080
1248 CGGGTTGTCTCCCGCAGATGGCCACAGAGGATAGCTTGAAGGTGGAGCTCATTTGGTTGC 1307
1081 CAGATTACCAAGGTAATGATTCATTTGGTGTGGCGCAAGCAAAAGTCAAAAGCACCAAGTGT 1140
1308 CAGATTACCAAGGTAATGATTCATTTGGTGTGGCGCAAGCAAAAGTCAAAAGCACCAAGTGT 1367
1141 TCAACTAAGAAAGAGATGAGCAATCAAGGCGCCATCCCTCGGAAGAAACATCCACA 1200
1368 TCAACTAAGAAAGAGATGAGCAATCAAGGCGCCATCCCTCGGAAGAAACATCCACA 1427
1201 GGAATTAACATTAACACGGTGGCTATTTCCATTTGGTGTCTCTTGTCTCTGTTGTTGCT 1260
1428 GGAATTAACATTAACACGGTGGCTATTTCCATTTGGTGTCTCTTGTCTCTGTTGTTGCT 1487
1261 GGAATGGGATCTTTGAGCCTTTAGAAAGAAAGAAAGAAAGTCCGTATGATCA 1320
1488 GGAATGGGATCTTTGAGCCTTTAGAAAGAAAGAAAGAAAGTCCGTATGATCA 1547
1321 GCGAGGCTCAGAAAACAGACTTGTGGAAGCAGATTAATATCCCTTTCGACACATCAG 1380
1548 GCGAGGCTCAGAAAACAGACTTGTGGAAGCAGATTAATATCCCTTTCGACACATCAG 1607
1381 TCAGCTGAGTTTACCATCAGCTATGATTAATGGAAGGAGATGACAAAAGTTAGATCTC 1440
1608 TCAGCTGAGTTTACCATCAGCTATGATTAATGGAAGGAGATGACAAAAGTTAGATCTC 1467
1441 ATCAAGTGTATGCGAGGTTA 1463
1668 ATCAAGTGTATGCGAGGTTA 1690

RESULT 15

US-09-814-353-20367

; Sequence 20367, Application US/09814353

; Publication No. US20030165831A1

; GENERAL INFORMATION:

; APPLICANT: Lee, John

; APPLICANT: Thompson, Pamela

; APPLICANT: Lillie, James

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

; FILE REFERENCE: MRI-006B

; CURRENT APPLICATION NUMBER: US/09/814,353

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: US 60/191,031

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: US 60/207,124

; PRIOR FILING DATE: 2000-05-25

; PRIOR APPLICATION NUMBER: US 60/211,940

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: US 60/216,820

; PRIOR FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: US 60/220,661

; PRIOR FILING DATE: 2000-07-25

; PRIOR APPLICATION NUMBER: US 60/257,672

; PRIOR FILING DATE: 2000-12-21

; NUMBER OF SEQ ID NOS: 22037

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 20367

; LENGTH: 3676

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: 3676

; OTHER INFORMATION: n = A,T,C or G

; US-09-814-353-20367

Query Match 99.7%; Score 1459.8; DB 3; Length 3676;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTTCGAAAGACAATT 60
DB 294 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTTCGAAAGACAATT 353
QY 61 ACAGTACCAAGGGGAAAAGACTGATTTCTGAGTTGGGAGATTTGATATCGAATCCCAG 120
DB 354 ACAGTACCAAGGGGAAAAGACTGATTTCTGAGTTGGGAGATTTGATATCGAATCCCAG 413
QY 121 ACCTGTGCTTCTGACTATCTTCTTCCAGCTCTTCCAGATCAATATGTTCCATATCTGT 180
DB 414 ACCTGTGCTTCTGACTATCTTCTTCCAGCTCTTCCAGATCAATATGTTCCATATCTGT 473
QY 181 GGAAGTATGACTGTTTCCCAAGAACTCTTGTGGAACACAAGTGAAGTAAACCGTCCGCTTT 240
DB 474 GGAAGTATGACTGTTTCCCAAGAACTCTTGTGGAACACAAGTGAAGTAAACCGTCCGCTTT 533
QY 241 GAGAGTGAATCCCAATTTCTGCGCGGGGTTTTTGTCTGACCTTATCGGAGCAGCAGCAT 300
DB 534 GAGAGTGAATCCCAATTTCTGCGCGGGGTTTTTGTCTGACCTTATCGGAGCAGCAGCAT 593
QY 301 CCAGATTTAATAACATGTTTGAACGAGCTAGCCATATTTGAAGACAGAATAACAGCAAA 360
DB 594 CCAGATTTAATAACATGTTTGAACGAGCTAGCCATATTTGAAGACAGAATAACAGCAAA 653
QY 361 TTCTGCCAGCTGTTGTAGAGACCTAGCAGAGACATTTCTGGGAATATGTTAGATGGA 420
DB 654 TTCTGCCAGCTGTTGTAGAGACCTAGCAGAGACATTTCTGGGAATATGTTAGATGGA 713
QY 421 TATAGAGATACCTCTTTTATTGTGCAAGCTGCCATCCATGCGAGGAATAATTTGCTGATGAA 480
DB 714 TATAGAGATACCTCTTTTATTGTGCAAGCTGCCATCCATGCGAGGAATAATTTGCTGATGAA 773
QY 481 CTAGTGGCCAGATCAGTGTGTTTTCAGCGCAAGGGATCAGTCGATATGAAGGATTTCTG 540

Db 774 CTAGGTGGCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATGAAGGGATTCTG 833
Qy GCCAATGGTGTCTTTTCAGGGATGGTTCCTGTCTCAGACAAGCGATTTCTGTTTACCTCC 600
Db 834 GCCAATGGTGTCTTTTCAGGGATGGTTCCTGTCTCAGACAAGCGATTTCTGTTTACCTCC 893
Qy 601 AATGGTTGCAGCAGATCCTTTGAGTTTTGAACTTGACGGGCAATCAGAGCTTCTTCTCA 660
Db 894 AATGGTTGCAGCAGATCCTTTGAGTTTTGAACTTGACGGGCAATCAGAGCTTCTTCTCA 953
Qy 661 TGGCAGTCCGTCAATGAGAGTGGAGACCAAGTTTCACTGGTCTCTGGCCCAAGCCGACTT 720
Db 954 TGGCAGTCCGTCAATGAGAGTGGAGACCAAGTTTCACTGGTCTCTGGCCCAAGCCGACTT 1013
Qy 721 CAGGACCAAGGCCCATCATCGGCTTCGGGCGACAGTAGCAACAACCAACCAACCGAGAG 780
Db 1014 CAGGACCAAGGCCCATCATCGGCTTCGGGCGACAGTAGCAACAACCAACCAACCGAGAG 1073
Qy 781 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAAGATCT 840
Db 1074 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAAGATCT 1133
Qy 841 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAACAATAAT 900
Db 1134 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAACAATAAT 1193
Qy 901 TCTAAGTGAAGACCTTATAAGGAATTTGTGAATAATGAAGAAAAGGTGTTTCAGGGTAAC 960
Db 1194 TCTAAGTGAAGACCTTATAAGGAATTTGTGAATAATGAAGAAAAGGTGTTTCAGGGTAAC 1253
Qy 961 TCTAACTTTTCGGGACCCAGTGCAAAACAATTTTCATCCCTCCATCGTGGCCAGATATGTG 1020
Db 1254 TCTAACTTTTCGGGACCCAGTGCAAAACAATTTTCATCCCTCCATCGTGGCCAGATATGTG 1313
Qy 1021 CGGGTTGTCCTCCAGACATGGCACCGAGATAGCTTTGAAGTGGAGCTCATTTGGTTGC 1080
Db 1314 CGGGTTGTCCTCCAGACATGGCACCGAGATAGCTTTGAAGTGGAGCTCATTTGGTTGC 1373
Qy 1081 CAGATTACACAAGTAAATGATTCATTGGTGTGGCGCAAGACAAGTCAAAGCACCAGTGT 1140
Db 1374 CAGATTACACAAGTAAATGATTCATTGGTGTGGCGCAAGACAAGTCAAAGCACCAGTGT 1433
Qy 1141 TCAACTAAGAAAGAAGATGAGACAATCAAGAAGCCCATCCCTCGGAAGAAAATCCACA 1200
Db 1434 TCAACTAAGAAAGAAGATGAGACAATCAAGAAGCCCATCCCTCGGAAGAAAATCCACA 1493
Qy 1201 GGAATRAACATTACAAGTGGCTATTCCATTGGTGTCTCTTGTGCTCTGGTGTGTGCT 1260
Db 1494 GGAATAAACATTACAAGTGGCTATTCCATTGGTGTCTCTTGTGCTCTGGTGTGTGCT 1553
Qy 1261 GGAATGGGATCTTTTCAGCCTTTTAGAAAGAAGAAGAAGGAAGTCCGTATGGATCA 1320
Db 1554 GGAATGGGATCTTTTCAGCCTTTTAGAAAGAAGAAGAAGGAAGTCCGTATGGATCA 1613
Qy 1321 GCGAGGCTCAGAAAACAAGACTGTGGAGCAGATTAAATATCCCTTTGCCAGACATCAG 1380
Db 1614 GCAGAGGCTCAGAAAACAAGACTGTGGAGCAGATTAAATATCCCTTTGCCAGACATCAG 1673
Qy 1381 TCAGCTCAGTTTACCATCAGCTATGATAATGAGAAGGAGATGACACAAAAGTTAGATCTC 1440
Db 1674 TCAGCTCAGTTTACCATCAGCTATGATAATGAGAAGGAGATGACACAAAAGTTAGATCTC 1733
Qy 1441 ATCAAGTGTATGGCAGTTA 1463
Db 1734 ATCAAGTGTATGGCAGTTA 1756

Search completed: January 15, 2006, 19:46:31
Job time : 1129 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2006, 19:53:27 ; Search time 949 Seconds
(without alignments)

4243.611 Million cell updates/sec

Title: US-10-813-588-2

Perfect score: 2557

Sequence: 1 MTSKNYPGTYPNHTVCEKTI.....YDNEKEMTKQLDLITSDMAG 487

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134683005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n model -DRV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10813588/runat_12012006_171132_15445/app_query.fasta_1.647
-DB=Published Applications NA_Main -QFMT=fastap -SUFFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10813588 @CGN_1_1549 @runat_12012006_171132_15445 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA_Main:

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2557	100.0	1464	9 US-10-813-588-1	Sequence 1, Appli
2	2557	100.0	1620	9 US-10-813-588-5	Sequence 5, Appli
3	2557	100.0	1761	6 US-10-295-027-1083	Sequence 1083, Ap
4	2557	100.0	1761	9 US-10-813-588-3	Sequence 3, Appli
5	2557	100.0	1768	9 US-10-813-588-7	Sequence 7, Appli
6	2557	100.0	2010	6 US-10-295-027-1082	Sequence 1082, Ap
7	2557	100.0	2010	8 US-10-783-528-23	Sequence 23, Appli

8	2557	100.0	2010	8	US-10-783-528-24	Sequence 24, Appli
9	2551	99.8	2145	3	US-09-759-1308-72	Sequence 72, Appli
10	2551	99.8	2145	7	US-10-741-790-72	Sequence 72, Appli
11	2551	99.8	2888	7	US-10-312-352-47	Sequence 47, Appli
12	2551	99.8	3151	5	US-10-003-132-1	Sequence 1, Appli
13	2551	99.8	3594	3	US-09-759-1308-71	Sequence 71, Appli
14	2551	99.8	3594	7	US-10-741-790-71	Sequence 71, Appli
15	2551	99.8	3676	3	US-09-814-353-20367	Sequence 20367, A
16	2512.5	98.3	2547	6	US-10-108-260A-999	Sequence 999, App
17	2259	88.3	2310	6	US-10-108-260A-999	Sequence 1084, Ap
18	2020	79.0	2145	5	US-10-003-132-12	Sequence 12, Appli
19	1313.5	51.4	1538	7	US-10-138-588-69	Sequence 69, Appli
20	1154.5	45.2	2836	5	US-10-003-132-3	Sequence 3, Appli
21	1146.5	44.8	1871	3	US-09-823-038A-43	Sequence 43, Appli
22	1003	39.2	2473	6	US-10-108-260A-2375	Sequence 2375, Ap
23	989	38.7	636	7	US-10-138-588-71	Sequence 71, Appli
24	974	38.1	596	8	US-10-696-639-1823	Sequence 1823, Ap
25	920	36.0	2868	5	US-10-003-132-5	Sequence 5, Appli
26	881.5	34.5	1509	5	US-10-003-132-13	Sequence 13, Appli
27	867.5	33.9	2310	6	US-10-191-436-7	Sequence 7, Appli
28	867.5	33.9	2310	6	US-10-191-436-9	Sequence 9, Appli
29	867.5	33.9	2310	10	US-11-055-679-7	Sequence 7, Appli
30	867.5	33.9	2310	10	US-11-055-679-9	Sequence 9, Appli
31	860.5	33.7	2190	5	US-10-060-830-2	Sequence 2, Appli
32	860.5	33.7	2280	5	US-10-060-830-1	Sequence 1, Appli
33	860.5	33.7	2328	6	US-10-191-436-1	Sequence 1, Appli
34	860.5	33.7	2328	6	US-10-191-436-3	Sequence 3, Appli
35	860.5	33.7	2328	10	US-11-055-679-1	Sequence 1, Appli
36	860.5	33.7	2328	10	US-11-055-679-3	Sequence 3, Appli
37	860.5	33.7	5657	3	US-09-974-298-96	Sequence 96, Appli
38	860.5	33.7	5657	5	US-10-084-817-65	Sequence 65, Appli
39	860.5	33.7	6595	8	US-10-723-860-6505	Sequence 6505, Ap
40	856.5	33.5	2310	6	US-10-191-436-4	Sequence 4, Appli
41	856.5	33.5	2310	6	US-10-191-436-6	Sequence 6, Appli
42	856.5	33.5	2310	10	US-11-055-679-4	Sequence 4, Appli
43	856.5	33.5	2310	10	US-11-055-679-6	Sequence 6, Appli
44	842.5	32.9	2200	7	US-10-451-010-13	Sequence 13, Appli
45	838	32.8	2428	5	US-10-106-698-1947	Sequence 1947, Ap

ALIGNMENTS

RESULT 1

US-10-813-588-1
; Sequence 1, Application US/10813588
; Publication No. US20050053969A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0071-USA
; CURRENT APPLICATION NUMBER: US/10/813,588
; CURRENT FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: US/09/691,344
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/183,583
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-813-588-1

Alignment Scores:

Pred. No.:	1.47e-292	Length:	1464
Score:	2557.00	Matches:	487
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-813-588-2 (1-487) x US-10-813-588-1 (1-1464)			
QY	1	MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluYsThrIle	20
DB	1	ATGACATCTAAGAAATATATCCGGGACCTACCCCAATCAACACTCTTTGGGAAAGACAAAT	60
QY	21	ThrValProLysGlyLysArgLeuLeuLeuArgLeuGlyAspLeuAspIleGluSerGln	40
DB	61	ACAGTACCAAGGGGAAAGACTGATCTGAGGTTGGAGATTGGATATCGAATCCCG	120
QY	41	ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys	60
DB	121	ACCTGTGCTTCTGACTATCTTCTTCACAGCTCTTCAGATCAATATGGTCCATACTGT	180
QY	61	GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe	80
DB	181	GGAAGTATGACTGTTCCCAAGAACTCTTGTGACACAACTGAAGTAAACCGTCCGCTT	240
QY	81	GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis	100
DB	241	GAGAGTGGATCCACATTTCTGGCGGGGTTTTTGTGACCTATGCGAGCAGCACCAT	300
QY	101	ProAspLeuIleThrCysLeuGluLeuArgAlaSerHisTyrLeuYsThrGluTyrSerLys	120
DB	301	CCAGATTAAATACATGTTTGGAAAGAGCTTAGCCATTTATTTGAAGACAGAAATACAGCAA	360
QY	121	PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly	140
DB	361	TTCTGCCAGCTGGTGTAGAGAGCTAGCAGGAGACATTTCTGGGAATATGGTAGATGA	420
QY	141	TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleLeuAlaAspGlu	160
DB	421	TATAGAGATACCTCTTTATTGTGCMAAGCTGCCATCCATCCAGGAAATATTCGTGATGA	480
QY	161	LeuGlyGlyGlnIleSerValLeuGlnArgGlyIleSerArgTyrGluGlyIleLeu	180
DB	481	CTAGGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATGAAGGGAATCTG	540
QY	181	AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer	200
DB	541	GCCAAATGGTGTCTTTTCGAGGATGGTTCCTGTGCAGCAAGCGAATTCGTTTACCTCC	600
QY	201	AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer	220
DB	601	AATGGTTGCAGCAGATCCTTGGATTTTGAACCTGACCGGCAAAATCAGAGCTTCTTCCTCA	660
QY	221	TrpGlnSerValhGlnSerGlyAspGlnValHisTrpSerProGlyGlnAlaAspLeu	240
DB	661	TGGCAGTCGGTCAATGAGTGGAGACCAAGTTCACCTGCTCTCGCCCAAGCCCGACTT	720
QY	241	GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu	260
DB	721	CAGACCAAGGCCCATCATGGGCTTCGGCGGACAGTAGCAACCAACCAACCCAGAGAG	780
QY	261	TrpLeuGlnLeuAspLeuGlyGluLysLysIleThrGlyIleArgThrThrGlySer	280
DB	781	TGGCTGGAGATCGATTTGGGGGAGAAAAAATAACAGGAATTAGGACCAACAGGATCT	840
QY	281	ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn	300
DB	841	ACACAGTCGAACCTTCAACTTTATGTAAAGAGTTTGTGATGAACCTTCAAAACCAATAT	900
QY	301	SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn	320
DB	901	TCTAAGTGGAGACCTATAAGGAATTTGTAATTAATGAAGAAAGGTTTCAGGGTAAC	960

QY	321	SerAsnPheArgAspProValGlnhAsnAsnPheIleProProIleValAlaArgTyrVal	340
DB	961	TCTAACTTTCCGGGACCCAGTGCAGAAACAATTTTCATCCCTCCCATCGTGGCCAGATATGT	1020
QY	341	ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys	360
DB	1021	CGGGTTGTCGCCAGACATGGCACCGAGAGTAGCTTGAAGTGGAGCTCAITGGTTGC	1080
QY	361	GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal	380
DB	1081	CAGATTACAAAGGTAATGATTCATTTGGTGTGGCGCAAGCAAGTCAAAAGCACCAGTGT	1140
QY	381	SerThrLysGluAspGluThrIleThrArgProIleProSerSerGluThrSerThr	400
DB	1141	TCAACTTAAGAAAGAGATGAGCAATCAAGGCCCATCCCTCGGAAGAAACATCCACA	1200
QY	401	GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValLeuValPheAla	420
DB	1201	GGATTAACAATTCACACGGTGGCTATTCATTTGGTGCTCTCTGTGCTGGTGTGCT	1260
QY	421	GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysGlySerProTyrGlySer	440
DB	1261	CGAATGGGATCTTTGCAGCCTTTAGAAAGAAAGAAAGAAAGTCCGTATGGATCA	1320
QY	441	AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln	460
DB	1321	CGGGAGGCTCAGAAAAACAGACTGTTGGAAGCAGATTAAATATATCCCTTTCGACACATCAG	1380
QY	461	SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu	480
DB	1381	TCAGCTGAGTTTACCATCAGCTATGATATAGAGAGAGATGACACAAAAGTTAGATCTC	1440
QY	481	IleThrSerAspMetAlaGly	487
DB	1441	ATCACAAGTGATATGGCAGGT	1461

RESULT 2

US-10-813-588-5

Sequence 5, Application US/10813588

Publication No. US20050053969A1

GENERAL INFORMATION:

APPLICANT: Donoho, Gregory

APPLICANT: Turner, C. Alexander Jr.

APPLICANT: Nehls, Michael

APPLICANT: Friedrich, Glenn

APPLICANT: Zambrowicz, Brian

APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: Novel Human Proteins and Polynucleotides

TITLE OF INVENTION: Encoding the Same

FILE REFERENCE: LEX-0071-USA

CURRENT APPLICATION NUMBER: US/10/813,588

CURRENT FILING DATE: 2004-03-30

PRIOR APPLICATION NUMBER: US/09/691,344

PRIOR FILING DATE: 2000-10-18

PRIOR APPLICATION NUMBER: US 60/160,285

PRIOR FILING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: US 60/183,583

PRIOR FILING DATE: 2000-02-18

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 1620

TYPE: DNA

ORGANISM: homo sapiens

US-10-813-588-5

Alignment Scores:	1.73e-292	Length:	1620
Score:	2557.00	Matches:	487
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-813-588-2 (1-487) x US-10-813-588-5 (1-1620)

QY 1 MetThrSerIysAsnTyrProGlyThrTyrProAsnHisThrValCysGluIysThrIle 20
DB 157 ATGACATCTAAGAAATTAATCCGGGAGCTACCCCAATCACACTGTGTTGCCGAAAGACAATT 216
QY 21 ThrValProIysGlyIysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 217 ACAGTACCAAGGGGAAGAGACTGATCTGAGGTTGGGAGATTTGGATATCGATATCCAG 276
QY 41 ThrCysAlaSerAspTyrIleLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
DB 277 ACCGTGCTTCTGACTATCTCTCTTACCAGCTCTTCAGATCAATATGGTCCATCTGT 336
QY 61 GlySerMetThrValProIysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
DB 337 GGAAGTATGACTGTTCCTCCCAAGAACTCTTGTGTAACACAGTGAAGTAAACCGTCCGCTTT 396
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 397 GAGAGTGGATCCACATTTCTGGCCGGGTTTTTGTGACCTATGCGAGCGAGACCAT 456
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuIysThrGluTyrSerLys 120
DB 457 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCATTTATGAAGACACAGATACAGCAAA 516
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 517 TTCTGCCAGCTGGTTGTAGACGCTAGCAGGAGACATTTCTGGGAATATGGTAGTGA 576
QY 141 TyrArgAspThrSerLeuLeuCysIysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
DB 577 TATAGATACCTCTTATTTGTGCAAGCTGCCATCCATGCGAGGAATATTTGCTGATGA 636
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
DB 637 CTAGGTGGCCAGATCAGTGTCTTACGCCAAAGGATCAGTCGATATGAAGGATTCGT 696
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB 697 GCCAATGGTGTCTTTTCGAGGAGATGGTTCCCTGTACAGCAAGCGATTTCTGTGTACCTCC 756
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
DB 757 ANTGGTTGAGCAGATCCTTGAGTTTGAACCTGCGGCAATCAGAGCTTCTCTCTCA 816
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 817 TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTCACTGTCTCTTGGCCCAAGCCGACTT 876
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 877 CAGAACCAAGGCCCATCATGGGCTTGGGCGCAGTAGCAACCAACCAACCAACGAGAG 936
QY 261 TrpLeuGluIleAspLeuGlyGlyIysLysIleThrGlyIleArgThrThrGlySer 280
DB 937 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAAGATCT 996
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
DB 997 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTTTGTGATCACTTCAAAAACAATAAT 1056
QY 301 SerLysTrpLysThrTyrIysGlyIleValAsnAsnGluIysValPheGlnGlyAsn 320
DB 1057 TCTAAGTGGAGACCTTATAAGGAATTGTGAATAATGAAGAAAAGGTGTTTCAGGGTAA 1116
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
DB 1117 TCTAATCTTGGGACCCAGTGCAGAAACAATTTCACTCCCTCCCATGTGGCCAGATATGG 1176
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360

DB 1177 CGGGTTGTCCTCCCGACAGATGGCACCAGAGATAGCCCTTGAAGGTGGAGCTCATTTGGTGC 1236
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
DB 1237 CAGATTACACAAGGTAATGATTTCATTTGGTGTGGCGCAAGACAAGTCAAGCACCAGTGT 1296
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
DB 1297 TCACTTAAGAAAGAGATGAGCAATCACAGGCCCATCCCTCGGAAGAAACATCCACA 1356
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValLeuValPheAla 420
DB 1357 GGAATAAAACATTTACAACGGTGGCTATTCATTTGGTGTCTCTTGTCTGGTGTGTGCT 1416
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysGlySerProTyrGlySer 440
DB 1417 GGAATGGGGATCTTTGCAGCCTTTAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1476
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
DB 1477 GCGGAGGCTCAGAAAACAGACTGTGGAAAGCAGATTAAATATATCCCTTTGCCAGACATCAG 1536
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
DB 1537 TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAAGTTAGATCTC 1596
QY 481 IleThrSerAspMetAlaGly 487
DB 1597 ATCACAAGTGATATGGCAGGT 1617

RESULT 3
US-10-295-027-1083
; Sequence 1083, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 1083
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-1083

Alignment Scores:
  Score: 1.97e-292      Length: 1761
  Pred. No.: 2557.00    Matches: 487
  Percent Similarity: 100.00%  Conservative: 0
  Best Local Similarity: 100.00%  Mismatches: 0
  Query Match: 100.00%  Indels: 0
  DB: 6  Gaps: 0

US-10-813-588-2 (1-487) x US-10-295-027-1083 (1-1761)

QY 1 MetThrSerIysAsnThrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB 298 ATGACATCTAAGAAATATATCCGGGACCTACCCCAATCACACTGTTTGGGAAAGACAAT 357
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 358 ACAGTACCAAGGGGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCAG 417
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
DB 418 ACCTGTGCTCTGACTATCTCTCTTCCAGGCTCTTCAGATCAATATGTCATACTGT 477
QY 61 GlySerMetThrValProLysGluLeuLeuLeuLeuLeuLeuLeuLeuValThrValArgPhe 80
DB 478 GGAAGTATGACTGTTCCCAAGAACTCTTGTTGAACACAGTAGTAAGTAAACCGTCCGCTTT 537
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 538 GAGAGTGGATCCACATTTCTGCGGGGTTTTTGTGCTGACCTATGCGAGCAGGACCAT 597
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
DB 598 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTAATTTGAAGACAGAAATACAGCAA 657
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 658 TTTCTGCCACGCTGGTTGTAGACAGCTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 717
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
DB 718 TATAGAGATACCTCTTTATTTGTCAAGCTGCCATCCATCAGGAATAATTTGCTGATGA 777
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
DB 778 CTAGGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGGATCAGTCGATATGAAGGGATTCTG 837
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB 838 GCCAATGGTGTCTTTTCAGAGGATGGTTCCTGTGCAGCAAGCAATTTCTTTACCTCC 897
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSer 220
DB 898 AATGGTTGCAGCAGATCTCTTGAGTTTTTGAACCTGACGGCAATATCAGAGCTTCTTCCTCA 957
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 958 TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTTCACTGGTCTCTGTCGCAAGCCCGACTT 1017
QY 241 GluAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 1018 CAGACCAAGCCCATCATGGCTTCGGGCGACAGTAGCAACACCAACCAACGAGAG 1077
QY 261 TrpLeuGluIleAspLeuGlyGluLysLysIleThrGlyIleArgThrThrGlySer 280
DB 1078 TGGCTGGAGATCGATTTGGGGGAAAAAAGAAATAACAGAAATTAGGACCAACAGGATCT 1137
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300

; SEQ ID NO 1138
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-1083

Alignment Scores:
  Score: 1.97e-292      Length: 1761
  Pred. No.: 2557.00    Matches: 487
  Percent Similarity: 100.00%  Conservative: 0
  Best Local Similarity: 100.00%  Mismatches: 0
  Query Match: 100.00%  Indels: 0
  DB: 6  Gaps: 0

US-10-813-588-2 (1-487) x US-10-295-027-1083 (1-1761)

QY 1 MetThrSerIysAsnThrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB 298 ATGACATCTAAGAAATATATCCGGGACCTACCCCAATCACACTGTTTGGGAAAGACAAT 357
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 358 ACAGTACCAAGGGGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCAG 417
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
DB 418 ACCTGTGCTCTGACTATCTCTCTTCCAGGCTCTTCAGATCAATATGTCATACTGT 477
QY 61 GlySerMetThrValProLysGluLeuLeuLeuLeuLeuLeuLeuLeuValThrValArgPhe 80
DB 478 GGAAGTATGACTGTTCCCAAGAACTCTTGTTGAACACAGTAGTAAGTAAACCGTCCGCTTT 537
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 538 GAGAGTGGATCCACATTTCTGCGGGGTTTTTGTGCTGACCTATGCGAGCAGGACCAT 597
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
DB 598 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTAATTTGAAGACAGAAATACAGCAA 657
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 658 TTTCTGCCACGCTGGTTGTAGACAGCTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 717
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
DB 718 TATAGAGATACCTCTTTATTTGTCAAGCTGCCATCCATCAGGAATAATTTGCTGATGA 777
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
DB 778 CTAGGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGGATCAGTCGATATGAAGGGATTCTG 837
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB 838 GCCAATGGTGTCTTTTCAGAGGATGGTTCCTGTGCAGCAAGCAATTTCTTTACCTCC 897
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSer 220
DB 898 AATGGTTGCAGCAGATCTCTTGAGTTTTTGAACCTGACGGCAATATCAGAGCTTCTTCCTCA 957
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 958 TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTTCACTGGTCTCTGTCGCAAGCCCGACTT 1017
QY 241 GluAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 1018 CAGACCAAGCCCATCATGGCTTCGGGCGACAGTAGCAACACCAACCAACGAGAG 1077
QY 261 TrpLeuGluIleAspLeuGlyGluLysLysIleThrGlyIleArgThrThrGlySer 280
DB 1078 TGGCTGGAGATCGATTTGGGGGAAAAAAGAAATAACAGAAATTAGGACCAACAGGATCT 1137
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300

; SEQ ID NO 1138
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-1083

Alignment Scores:
  Score: 1.97e-292      Length: 1761
  Pred. No.: 2557.00    Matches: 487
  Percent Similarity: 100.00%  Conservative: 0
  Best Local Similarity: 100.00%  Mismatches: 0
  Query Match: 100.00%  Indels: 0
  DB: 6  Gaps: 0

US-10-813-588-2 (1-487) x US-10-295-027-1083 (1-1761)

QY 1 MetThrSerIysAsnThrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB 298 ATGACATCTAAGAAATATATCCGGGACCTACCCCAATCACACTGTTTGGGAAAGACAAT 357
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 358 ACAGTACCAAGGGGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCAG 417
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
DB 418 ACCTGTGCTCTGACTATCTCTCTTCCAGGCTCTTCAGATCAATATGTCATACTGT 477
QY 61 GlySerMetThrValProLysGluLeuLeuLeuLeuLeuLeuLeuLeuValThrValArgPhe 80
DB 478 GGAAGTATGACTGTTCCCAAGAACTCTTGTTGAACACAGTAGTAAGTAAACCGTCCGCTTT 537
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 538 GAGAGTGGATCCACATTTCTGCGGGGTTTTTGTGCTGACCTATGCGAGCAGGACCAT 597
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
DB 598 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTAATTTGAAGACAGAAATACAGCAA 657
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 658 TTTCTGCCACGCTGGTTGTAGACAGCTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 717
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
DB 718 TATAGAGATACCTCTTTATTTGTCAAGCTGCCATCCATCAGGAATAATTTGCTGATGA 777
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
DB 778 CTAGGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGGATCAGTCGATATGAAGGGATTCTG 837
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB 838 GCCAATGGTGTCTTTTCAGAGGATGGTTCCTGTGCAGCAAGCAATTTCTTTACCTCC 897
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSer 220
DB 898 AATGGTTGCAGCAGATCTCTTGAGTTTTTGAACCTGACGGCAATATCAGAGCTTCTTCCTCA 957
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 958 TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTTCACTGGTCTCTGTCGCAAGCCCGACTT 1017
QY 241 GluAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 1018 CAGACCAAGCCCATCATGGCTTCGGGCGACAGTAGCAACACCAACCAACGAGAG 1077
QY 261 TrpLeuGluIleAspLeuGlyGluLysLysIleThrGlyIleArgThrThrGlySer 280
DB 1078 TGGCTGGAGATCGATTTGGGGGAAAAAAGAAATAACAGAAATTAGGACCAACAGGATCT 1137
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
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Alignment Scores:

Pred. No.: 1,97e-292 Length: 1761
Score: 2557.00 Matches: 487
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-813-588-2 (1-487) x US-10-813-588-3 (1-1761)

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QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB 298 ATGACATCTAAGAAATTAATCCCGGACCTACCCCAATCACACTGTTTGGCAAGACAAT 357
QY 21 ThrValProLysGlyLysArgLeuLeuLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 358 ACAGTACCAAGGGGAAGAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCAG 417
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
DB 418 ACCTGTGCTTCTGACTATCTCTCTTCCAGAGCTCTTCCAGATCAATATGGTCCATCTGT 477
QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
DB 478 GGAAGTATGACTGTTCCCAAGAACTCTTTGTTGAACACAAAGTGAAGTAAACCGTCCGCTTT 537
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 538 GAGAGTGGATCCACATTTCTGGCCGGGGTTTTTGTGCTGACCTATCCGAGCAGCGACCAT 597
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
DB 598 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACACAAATACAGCAA 657
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 658 TTCTGCCAGCTGGTTGTAGACGCTAGCAGGAGACATTTCTGGGAATATGGTAGTGA 717
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleAlaAspGlu 160
DB 718 TATAGATACCTCTTATTTGGCAAGCTGCCATCCATCGAGGAATAATTTGCTGATGAA 777
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
DB 778 CTAGGTGGCCAGATCAGTGTCTTCCAGCAAGGGATCAGTCGATATCAAGGGATTCTG 837
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB 838 GCCAATGGTGTCTTTTCGAGGGATGGTTCCTGTCCAGACAGCGATTTCTGTTTACCTCC 897
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSer 220
DB 898 AATGTTGGACAGATCTCTTGAGTTTGAACCTGCGGGCAATCAGAGCTTCTTCCTCA 957
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 958 TGGCAGTGGTCAATGAGAGTGGAGACCAAGTTCACTGTCTCTCTGGCCCAAGCCGACTT 1017
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 1018 CAGGACCAAGGCCCATCATGGGCTTGGGGCGACGATAGCAACAAACCAACACGAGAG 1077
QY 261 TrpLeuGluIleAspLeuGlyLysLysLysIleThrGlyIleArgThrThrGlySer 280
DB 1078 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAAGATCT 1137
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
DB 1138 ACACAGTGAACCTCAACTTTTATGTTAAGAGTTTGTGATGACTTCAAAAACATAAT 1197
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
DB 1198 TCTAAGTGAAGACCTATAAGGAATTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAAC 1257
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QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
DB 1258 TCTAACTTTCCGGACCCAGTGCAAAACAATTTATCCCTCCCATCTGGGCCAGATATGTG 1317
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
DB 1318 CGGGTTGTCCCCACAGACATGGCAGAGGATAGCCTTGAAGGTGGAGCTCATTTGGTTGC 1377
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
DB 1378 CAGATTACCAAGGTAATGATTCAATTGGTGTGGCCGCAAGCAAGTCAAAAGCACCACTGT 1437
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
DB 1438 TCACACTAGAAAGAGATGAGACATCACAGGCCCATCCCTCGGAAGAAATCATCCACA 1497
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValPheAla 420
DB 1498 GGAATAAAACATTTACAACGGTGGCTATTCATTGGTGTCTCTTTGTTGCTGGTGTGCT 1557
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysGlySerProTyrGlySer 440
DB 1558 GGAATGGGGATCTTTGCAGCCTTTAGAAAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1617
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
DB 1618 GCGGAGGCTCAGAAACAGACTGTGGAGCAGATTAATATCCCTTTGCCAGACATCAG 1677
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
DB 1678 TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAGGAGATGACACAAAGTTAGATCTC 1737
QY 481 IleThrSerAspMetAlaGly 487
DB 1738 ATCACAAGTGATATGGCAGGT 1758
```

RESULT 5
US-10-813-588-7
; Sequence 7, Application US/10813588
; Publication No. US20050053969A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Proteins and Polynucleotides
; FILE REFERENCE: LEX-0071-USA
; CURRENT APPLICATION NUMBER: US/10/813,588
; PRIOR FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: US/09/691,344
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/183,583
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1768
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-813-588-7

Alignment Scores:
Pred. No.: 1,99e-292 Length: 1768
Score: 2557.00 Matches: 487
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

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DB:          9          0          Caps:
US-10-813-588-2 (1-487) x US-10-813-588-7 (1-1768)
QY    1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB    59 ATGACATCTTAAGAAATATCCGGGACCTACCCCAATCACACTGTTTGGCAAAAGACAAAT 118
QY    21 ThrValProGlySerGlyArgLeuLleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB    119 ACAGTACCAAGAGGGGAAAAGACTGATTCTGAGGTTGGGAGATTTGGATATCGAATCCCAAG 178
QY    41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
DB    179 ACCTGTGCTTCTGACTATCTCTCTTACCAGCTCTTCAGATCAATATGTTCCATACTGT 238
QY    61 GlySerMetThrValProLysGluLeuLeuLeuLeuLeuLeuLeuLeuLeuValThrValArgPhe 80
DB    239 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTAACACAACTGAGTAACCGTCCGCTTT 298
QY    81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB    299 GAGAGTGGATCCACATTTCTGGCCGGGTTTTTGTGACCTATCGAGCAGCGACCAT 358
QY    101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
DB    359 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTGGAAGACAGAAATACAGCAAA 418
QY    121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB    419 TTTGCCCGACTGGTTGTAGAGAGCTAGTACAGGAGACATTTCTGGGAATATGGTAGATGA 478
QY    141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
DB    479 TATAGAGATACCTCTTTATTGTGCNAAGCTGCCATGCAGCAATAATTGCTGATGAA 538
QY    161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
DB    539 CTAGGTGGCCAGATCATGATGTGCTTCAGCGCAAAAGGATCATGTCATATGAAGGATTCG 598
QY    181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB    599 GCCAATGGTGTTCTTCAGGAGATGTTCCTCTGTACAGCAAGCATTTCTGTTACTCTCC 658
QY    201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSer 220
DB    659 AATGGTTGCAGCAGATCTTGTAGTTTGAACCTGACGGCAATACAGAGCTTCTCTCTCA 718
QY    221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB    719 TGGCAGTCCGTCAATGAGAGTGGAGACCAAGTTCACTGGTCTCTGCGCAAGCCGACTT 778
QY    241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProAspGlu 260
DB    779 CAGACCAAGGCCCATCATCGGCTTCGGCGCAGTAGCAACCAACCAACCAACGAGAG 838
QY    261 TrpLeuGluIleAspLeuGlyGluLysLysLysIleThrGlyIleArgThrThrGlySer 280
DB    839 TGGCTGGAGATCGATTTGGGGGAGAAAAAATAACAGGAATTAGGACCAAGCATCT 898
QY    281 ThrGlnSerAsnPheAsnPheThrValLysSerPheValMetAsnPheLysAsnAsn 300
DB    899 ACACAGTCGAACCTTCAACTTTATGTATGAGAGTTTGTGATGAACCTTCAAAAAACAATAAT 958
QY    301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
DB    959 TCTAAGTGGGAACCTTAAGGAATTTGTGAATAATGAAGAAAGGTGTTTCAGGTTAAC 1018
QY    321 SerAsnPheArgAspProValGlnAsnAsnPheIleProPheValAlaArgTyrVal 340
DB    1019 TCTAACTTTTCGGGACCCAGTGCAAAACAATTTTCATCCCTCCATCGTGGCCAGATATGTG 1078
QY    341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
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RESULT 6

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US-10-295-027-1082
; Sequence 1082, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1082
LENGTH: 2010
TYPE: DNA
ORGANISM: Homo sapiens
US-10-295-027-1082

Alignment Scores:

Pred. No.: 2,446-292 Length: 2010
Score: 2557.00 Matches: 487
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-813-588-2 (1-487) x US-10-295-027-1082 (1-2010)

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QY 1 MetThrSerIysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB 282 ATGACATCTAAGAAATTATCCCGGACCTACCCCAATCACACTGTTTGGCAAAAGACAATT 341
QY 21 ThrValProLysGlyValArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 342 ACAGTACCAAGGGAAAGACTGATCTGAGGTTGGAGATTGGATATCGAATCCCCAG 401
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
DB 402 ACTGTGCTTCTGACTATCTCTCTTACCAGCTCTTCAGATCAATATGTCCTACTGT 461
QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
DB 462 GGAAGTATGACTGTTCCCAAGAACTCTTTGTTGAACACAAAGTGAAGTAAACCGTCGGCTTT 521
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 522 GAGAGTGGATCCACATTTCTGCGCGGGGTTTTTGTCTGACCTATGCGAGCGACCAAT 581
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
DB 582 CCAGATTTAATACATGTTTGGACGAGCTAGCCATTATTTGAGACAGATACAGCAAA 641
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 642 TTCTGCCAGCTGGTTGTAGACAGCTAGCAGAGACATTTCTGGGAATATGCTAGTGA 701
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
DB 702 TATAGAGATACCTCTTTATTTGCAAAAGCTGCCATCCATGCGAGGAATAATTGCTGATGA 761
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
DB 762 CTAGGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATGAAGGGATCTG 821
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB 822 GCCAATGGTGTCTTTTCGAGGGATGTTCCCTGTGACAGACGATTTCTGTTTACCTCC 881
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
DB 882 AATGGTTGCAGAGATCCTTTGAGTTTGAACCTGACGGGCAATCAGAGCTTCTTCCCTCA 941
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 942 TGGCAGTCCGTCAATGAGATGGAGNCCCAAGTTCACTGTCTCTGCGCAACCCGACTT 1001
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 1002 CAGGACCAAGGCCCATCATGGGCTTCGGCGCAGTAGCAACCAACCAACCAACGAGAG 1061
QY 261 TrpLeuGluIleAspLeuGlyGluLysLysLysIleThrGlyIleArgThrThrGlySer 280
DB 1062 TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAATAACAGGAATTAGGACCAACGAGTCT 1121
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QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
DB 1122 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTTTGATGACTTCAAAACATAT 1181
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn 320
DB 1182 TCTAAGTGAAGACCTATAAAGGAATTGTGAATAATAGAAAAAGGTGTTTCAGGGTAAC 1241
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
DB 1242 TCTAACTTTTCGGGACCCAGTGCAAAACAATTTTCATCCCTCCCATCGTGCCAGATATGG 1301
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
DB 1302 CGGGTTGTCCTCCACAGCATGGCCAGAGGATAGCTTTGAAGGTGGAGCTCATTTGGTTGC 1361
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
DB 1362 CAGATTACAAAGGTAATGATTCAATTGTTGTGGCGCAAGACAAGTCAAAAGCACCACTGTT 1421
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
DB 1422 TCACTTAAGAAAGAAGATGAGACAATCAAGGCCCATCCCTCGAAGAAACATCCACA 1481
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValPheAla 420
DB 1482 GGAATTAACATTTACAACGGTGGCTATTTCATTGGTGTCTCTTGTGCTCTGCTGTTGCT 1541
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysLysLysLysLys 440
DB 1542 GGAATGGGGATCTTTGCGAGCCTTTAGAAAAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1601
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
DB 1602 GCAGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAATAATATCCCTTTGCCAGACATCAG 1661
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
DB 1662 TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAAGTTAGATCTC 1721
QY 481 IleThrSerAspMetAlaGly 487
DB 1722 ATCACAAGTGATATGGCAGGT 1742
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RESULT 7

US-10-783-528-23
Sequence 23, Application US/10783528
Publication No. US20040219579A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Gish, Kurt
APPLICANT: Wilson, Keith
APPLICANT: Zlotnick, Albert
TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
FILE REFERENCE: 05882.0191.NPUS01
CURRENT APPLICATION NUMBER: US/10/783,528
CURRENT FILING DATE: 2004-02-19
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 2010
TYPE: DNA
ORGANISM: Homo sapiens
US-10-783-528-23

Alignment Scores:
Pred. No.: 2,446-292 Length: 2010
Score: 2557.00 Matches: 487
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-813-588-2 (1-487) x US-10-783-528-23 (1-2010)

QY 1 MetThrSerIysAsnTyrProGlyThrTyrProAsnHisThrValCysGluIysThrIle 20
DB 282 ATGACATCTAAGAAATATCCGGGACCTACCCCAATCACACTGTTTGGCAAGAAACAAT 341
QY 21 ThrValProIysGlyIysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 342 ACAGTACCAAGGGGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCCGAG 401
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
DB 402 ACCTGTCCTTCTGACTATCTCTCTCACCGGCTCTTCAGATCAATATGTCCTACTGT 461
QY 61 GlySerMetThrValProIysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
DB 462 GGAAGTATGACTGTTCCCAAGAACTCTTGTTGAACACAACTGAACTAACCGTCCGCTTT 521
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 522 GAGAGTGGATCCACATTTCTGGCCGGGGTTTTTGTGACCTATTCGAGCAGCGACCAT 581
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuIysThrGluTyrSerLys 120
DB 582 CCAGATTATAACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGATACACAAA 641
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 642 TTCTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 701
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
DB 702 TATAGAGATACCTCTTTATTGTGAAAGCTGCCATCATCATGAGAAATAATTGCTGATGA 761
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
DB 762 CTAGTGGCCAGATCAGTGTCTTCAGCGCAAGGGATCAGTCGATATGAGGGATCTCG 821
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB 822 GCCAATGGTGTCTTTCCGAGGATGGTTCCCTGTGCAGACAAGCGATTTCTGTTTACTCTC 881
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
DB 882 AATGGTTGCAGCAGATCCTTGAGTTTGAACCTTGACGGCAATTCAGAGCTTCTTCTCTCA 941
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 942 TGGCAGTTCGTCAATGAGATGGAGACCAAGTTCACTGGTCTCTGCGCAAGCCGACCTT 1001
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnHisLysProArgGlu 260
DB 1002 CAGGACCAAGGCCCATCATGGCTTCGGCGCACAGTAGCAACAACCAACCAACGAGAG 1061
QY 261 TrpLeuGluIleAspLeuGlyGluLysLysIleThrGlyIleArgThrThrGlySer 280
DB 1062 TGGCTGGAGATCGAATTTGGGGGAAAGAAATAACAGGAATTTAGGACACAGAGATCT 1121
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
DB 1122 ACAGTTCGAACTTCACTTTTATGTTAAGGTTTGTGATGAACTTCAAAAACATAAT 1181
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn 320
DB 1182 TCTAAGTGAAGACCTATAAGGAATTTGTGAATAATGAAGAAAGGTTTTCAGGGTAAC 1241
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProPheIleValAlaArgTyrVal 340
DB 1242 TCTAATCTTCGGGACCCAGTGCAAAACAATTTTCACTCCCTCCATCGGGCAGATATGT 1301
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
DB 1302 CGGGTTGTCCCCCAGACATGGCACCGAGGATAGCCCTTGAAGGTGGAGCTCATTTGGTTGC 1361

RESULT 8

US-10-783-528-24
; Sequence 24, Application US/10783528
; Publication No. US20040219579A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataasha
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
; FILE REFERENCE: 05882.0191.NPUS01
; CURRENT APPLICATION NUMBER: US/10/783,528
; CURRENT FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-783-528-24

Alignment Scores:
Pred. No.: 2,44e-292 Length: 2010
Score: 2557.00 Matches: 487
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-813-588-2 (1-487) x US-10-783-528-24 (1-2010)

QY 1 MetThrSerIysAsnTyrProGlyThrTyrProAsnHisThrValCysGluIysThrIle 20
DB 282 ATGACATCTAAGAAATATCCGGGACCTACCCCAATCACACTGTTTGGCAAGAAACAAT 341
QY 21 ThrValProIysGlyIysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 342 ACAGTACCAAGGGGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCCGAG 401
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
DB 402 ACCTGTCCTTCTGACTATCTCTCTCACCGCTTCAGATCAATATGTCCTACTGT 461
QY 61 GlySerMetThrValProIysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80

Db 462 GGAAGTATGACTCTTCCCAAGAACTCTTGTGAACACAACTGAAGTAAACCGTCCGCTTT 521
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyralaSerSerAspHis 100
Db 522 GAGAGTGGATCCCACTTTCTGCCCGGGTTTTTCTGCTACCTATCGAGCAGCACCAT 581
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrluLeuLysThrGluTyrluSerLys 120
Db 582 CCAGATTTAATACATGTTTGAACGAGCTAGCCATTATTGAAGACAGATACACAAA 641
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
Db 642 TTCCTGCCAGCTGTTGTAGACAGCTAGCAGAGACATTTCTGGGAATATGGTAGATGA 701
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
Db 702 TATAGAGATACCTCTTTATTTGTCAAGCTGCCATCCATCGAGGAATAATTGCTGATGAA 761
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrluGluGlyIleLeu 180
Db 762 CTAGGTGGCCAGATCAGTGTCTTCAGCGCAAGGGATCAGTCGATATGAGGGATTCTG 821
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
Db 822 GCCAATGGTGTCTTTTCGAGGGATGTTCCCTGTCCAGACAAGCCATTTCTGTTTACCTCC 881
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
Db 882 AATGGTGTGACAGATCCTTTGAGTTTGAACCTGACGGGCAATCAGAGCTTCTTCTCTCA 941
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
Db 942 TGGCAGTGGTCAATGAGAGTGGAGACCAAGTTCACTGTCTCTGCTGCCAAGCCGACTT 1001
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
Db 1002 CAGCAACCAAGGCCATCATGGGCTTCGGCGCAGTAGCAACAACCAACAACCAAGAG 1061
QY 261 TrpLeuGluIleAspLeuGlyGluLysLysLysIleThrGlyIleArgThrThrGlySer 280
Db 1062 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCCAGAGATCT 1121
QY 281 ThrGlnSerAsnPheAsnPheTyrluValLysSerPheValMetAsnPhelysAsnAsn 300
Db 1122 ACACAGTCCGACTTCACTTTATGTAAAGATTTTGTGATGACTTCAAAACCAATAT 1181
QY 301 SerLysTrpLysThrTyrluLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn 320
Db 1182 TCTAAGTGAAGACCTTAAAGGAATTTGTAATATGAAGAAAAGGTGTTTCAGGGTAAC 1241
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrluVal 340
Db 1242 TCTAAGTTCGGGACCCAGTGAACAAATTTTCATCCCTCCATCGTGCCAGATATGTG 1301
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
Db 1302 CGGGTGTCCCCAGACATGGCCAGAGATAGCTTGAAGGTGGAGCTCATTTGGTTGC 1361
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
Db 1362 CAGATTACAAAGGTAATGATTCATTTGTTGGCGCAGACAAGTCMAAGCACCAGTGT 1421
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
Db 1422 TCAACTAAGAAAGAGATGAGACAATCAAGAGCCCATCCCTCGGAAGAAATCCACCA 1481
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValLeuPheAla 420
Db 1482 GGAATAAACAATTACACGGTGGCTATTCATTTGGTGTCTCTTGTGCTCTGTTGTGT 1541
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysLysLysLysLys 440

Db 1542 GGAATGGGATCTTTGACGCTTTAGAAAAGAAAGAAAGAAAGTCCGTATGATCA 1601
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrluPheAlaArgHisGln 460
Db 1602 GCAGAGGCTCAAGAAACAGACTGTTGGAAGCAGATTAAATATATCCCTTTGCCAGACATCAG 1661
QY 461 SerAlaGluPheThrIleSerTyrluAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
Db 1662 TCAGCTGAGTTTACCATCAGCTATGATATAGAGAGGAGATGACACAAAAGTTAGATCTC 1721
QY 481 IleThrSerAspMetAlaGly 487
Db 1722 ATCACAAGTGATATGCGAGGT 1742

RESULT 9
US-09-759-130B-72
; Sequence 72, Application US/09759130B
; Publication NO. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES.
; FILE REFERENCE: MP100-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-130B-72

Alignment Scores:
Pred. No.: 1,396-291 Length: 2145
Score: 2551.00 Matches: 486
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 3 Gaps: 0

US-10-813-588-2 (1-487) x US-09-759-130B-72 (1-2145)

QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB 157 ATGACATCTAAGAAATTTATCCGGGACCTACCCCAATCACACTGTTTGGGAAAAGACAAT 216
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 217 ACAGTACCAGGAGGAAAAGACTGATCTGAGGTTGGGAGATTTGGATATCGAATCCGAG 276
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
DB 277 ACCTGTGCTCTGACTATCTCTCTTCCACAGGCTCTTCAGATCATATGCTCATCTGTT 336
QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
DB 337 GGAAGTATGACTGTTCCCAAGAACTCTTGTTGAAACACAAGTGAAGTAAACCGTCCGCTTT 396
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 397 GAGAGTGGATCCACATTTCTGGCCGGGTTTTTGTGACCTATTCGAGCAGCGACCAT 456
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
DB 457 CCAGATTTAATAACATGTTTGGAAACGAGCTAGGCCATTTATTTGAAGACAGATACGAAA 516
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 517 TTCTGCCAGCTGGTTGTAGAGAGCTAGCAGGAGACATTTCTCGGAATATGTTAGATGGA 576
QY 141 TyrArgAspThrSerLeuLeuLysLysAlaAlaIleHisAlaGlyIleLeuLeuLeu 160
DB 577 TATAGAGATACCTCTTTATTTGTCAAAAGCTGCCATCCATCGAGAAATATTTGCTGATGA 636
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
DB 637 CTAGGTGGCCAGATCAGTGTGCTTCACGGCAAAAGGATCAGTCATATGAAGGATCTCG 696
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB 697 GCCAATGGTGTCTTTCAGGGATGGTTCCCTGTCAGACAAGCGATTTCTGTTTACCTCC 756
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSer 220
DB 757 AATGGTTGCAGCAGATCTTGTAGTTTGTGAACCTGACGGCAAAATCAGAGCTTCTTCTCA 816
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 817 TGGCAGTCCGTCAATGAGAGTGAGACCAAGTTCACTGGTCTCTGCGCAAGCCGACCTT 876
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnHisLysProArgGlu 260
DB 877 CAGGACCAAGGCCCATCATGGCTTCCGGCGACAGTAGCAACAACCAACCAACAGAGAG 936
QY 261 TrpLeuGluIleAspLeuGlyLysLysValIleThrGlyIleArgThrThrGlySer 280
DB 937 TGGCTGGAGATCGAATTTGGGGGAGAAAAGAAAATAACAGAAATTAGGACCAAGATCT 996
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
DB 997 ACACAGTCGAACCTTCACTTTATTTGTTAAGAGTTTGTGATGAACCTTCAAAAACAATAT 1056
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
DB 1057 TCTAAGTGGAGAACCTATAAGGAATTTGTAATAATGAAGAAAGGTTTTCAGGGTAA 1116
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
DB 1117 TCTAACTTTTCGGGACCCAGTCGCAAAACAATTTTATCTCCCTCCATCGTGGCCAGATATGT 1176
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
DB 1177 CGGGTTGTCCTCCCGACATGGCACGAGGATAGCTTTGAAGTGGAGCTCATTTGTTGTC 1236

QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
DB 1237 CAGATTCACAAAGGTAATGATTCATTTGGTGGCGCAAGACAAGTCAAAAGCACAGTGT 1296
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
DB 1297 TCAACTAAGAAAAGAGATGAGACAATCAAGGCCCATCCCTCGGAAGAAACATCCACA 1356
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValPheAla 420
DB 1357 GGAATAACATTCACAAAGTGGCTATTCATTTGGTGTCTTGTGTTCTGCTGTTGCT 1416
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysGlySerProTyrGlySer 440
DB 1417 GCAATGGGGATCTTTTCAGCCCTTTAGAAAAGAAAGAAAGAAAGGAGTCCGTATGATCA 1476
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
DB 1477 GCAGAGGCTTCAGAAAACAGACTGTTGGAGCAGATTTAAATATCCCTTTGCCAGACATCAG 1536
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
DB 1537 TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAGGAGATGACACAAAAGTTAGATCTC 1596
QY 481 IleThrSerAspMetAla 486
DB 1597 ATCAACAAGTGATATGGCA 1614
RESULT 10
US-10-741-790-72
; Sequence 72, Application US/10741790
; Publication NO. US20040121396A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/10/741,790
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 72

LENGTH: 2145

TYPE: DNA

ORGANISM: Homo sapiens

US-10-741-790-72

Alignment Scores:

Pred. No.: 1-39e-291 Length: 2145
Score: 2551.00 Matches: 486
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 7 Gaps: 0

US-10-813-588-2 (1-487) x US-10-741-790-72 (1-2145)

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QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGlyLysThrIle 20
DB 157 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACACTGTTTGGCAAAAGACAATT 216
QY 21 ThrValProGlyGlyLysArgLysLysLysLysLysLysLysLysLysLysLysLys 40
DB 217 ACAGTACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 276
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
DB 277 ACTGTGCTTCTGACTATCTCTCTCACCACTCTTCAGATCAATATGCTGCTACTGT 336
QY 61 GlySerMetThrValProLysGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
DB 337 GGAAGTATGACTGTTCCCAAGAACTCTTTGTTGAACACAACTGAGTAACTGCTGCT 396
QY 81 GluSerGlySerHisLysSerGlyArgGlyPheLeuLeuLeuLeuLeuLeuLeuLeu 100
DB 397 GAGAGTGGATCCACATTTCTGCGCGGGTTTTTCTGCTGACCTATGCGAGCAGCCAT 456
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
DB 457 CCAGATTATTAACATGTTTGGNACGAGCTAGCCATTATTTGAGACAGACAGTACAGCAA 516
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspLysSerGlyAsnMetValAspGly 140
DB 517 TTCTGCCAGCTGGTTGTAGACAGCTAGCAGGAGACATTTCTGGGAATATGCTAGTGA 576
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyLysLysLysLys 160
DB 577 TATAGATATACCTCTTTATTTGCAAGCTGCCATCCATGCGAGGAAATATTTCTGATGA 636
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyLysArgTyrGluGlyLysLeu 180
DB 637 CTAGGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATGAAGGATCTG 696
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB 697 GCCAATGGTGTCTTTCGAGGGATGTTCCCTGTGAGCAAGCGATTTCTGTTTACCTCC 756
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
DB 757 AATGGTTCGAGCAGATCTTTAGTTTGAACCTGAGCGGCAATCAGAGCTTTCTTCTCTCA 816
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTyrSerProGlyGlnAlaArgLeu 240
DB 817 TGGCAGTGGTCAATGAGAGTGGAGCCCAAGTTCACTGCTCTCTGGCCACCCGACTT 876
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 877 CAGGACCAAGGCCCATCATGGGCTTCGGCGCAGCAGTAGCAACACCAACCAACGAGAG 936
QY 261 TrpLeuGluIleAspLeuGlyLysLysLysLysLysLysLysLysLysLysLysLys 280
DB 937 TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAAAAATACAGGAATTAGGACCAACAGGATCT 996
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QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
DB 997 ACACAGTCGAATCTTCACTTTTATGTTAAGAGTTTGTGATGAACATTCAAAACCAATAT 1056
QY 301 SerLysTyrLysThrTyrLysGlyLysValAsnAsnGluGluLysValPheGlnGlyAsn 320
DB 1057 TCTAAGTGGAGACCTATAAAGGAATTTGTAATATGAAGAAAGGTTTTCAGGGCTAAC 1116
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
DB 1117 TCTAACTTTTCGGGACCCAGTGCAGAACCAATTTTCATCCCTCCCATCGTGGCCAGATATG 1176
QY 341 ArgValValProGlnThrTyrHisGlnArgLysLysLysLysLysLysLysLysLys 360
DB 1177 CGGGTTGTCCTCCACAGCATGGCCAGAGGATAGCTTGAAGGTGGAGTCTCATTTGGTTGC 1236
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTyrArgLysThrSerGlnSerThrSerVal 380
DB 1237 CAGATTACACAGGTAATGATTCAATTTGGTGTGGCGCAGACAAAGTCAAAAGCACCACTGTT 1296
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
DB 1297 TCAACTAAGAAAGAGATGAGACAATCAAGAGCCCATCCCTCGGAGAAACATCCACA 1356
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValLeuValPheAla 420
DB 1357 GGAATTAACATTTACAAAGTGGTGTATTCATTTGGTGTCTCTTGTGCTCTGTTGTTGCT 1416
QY 421 GlyMetGlyLysPheAlaAlaPheArgLysLysLysLysLysLysLysLysLysLys 440
DB 1417 GGAATGGGATCTTTGACGCTTTAGAAAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1476
QY 441 AlaGluAlaGlnIleThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
DB 1477 GCAGAGGCTCAAGAAACAGACTGTTGGAAGCAGATTAATATATATCCCTTTGCCAGACATCAG 1536
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
DB 1537 TCAGCTGAGTTTACCATCAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1596
QY 481 IleThrSerAspMetAla 486
DB 1597 ATCACAAGTGATATGGCA 1614
RESULT 11
US-10-312-352-47
; Sequence 47, Application US/10312352
; Publication No. US20040053824A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom
; APPLICANT: YUE, Henry; AZIMZAI, Yalda
; APPLICANT: HE, Ann; BATRA, Sajeev
; APPLICANT: LO, Terence P.; NGUYEN, Danniell B.
; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
; APPLICANT: ZINGLER, Kurt A.; GANDHI, Ameena R.
; APPLICANT: LAL, Preeti G.; KEARNEY, Liam
; APPLICANT: BURFORD, Neil; YAO, Monique G.
; APPLICANT: CHAWLA, Narinder K.; ELLIOT, Vicki S.
; APPLICANT: ARVIZU, Chandra S.; KHAN, Farrah A.
; APPLICANT: BAUGHN, Mariah R.; HAPALIA, April, J.A.
; APPLICANT: POLICKY, Jennifer L.; AU-YOUNG, Janice K.
; APPLICANT: LU, Yan; BOROMSKY, Mark L.
; APPLICANT: LU, Dying Aina M.; RAMKUMAR, Jayalaxmi
; APPLICANT: YANG, Junming; GURURAJAN, Rajagopal
; APPLICANT: WARREN, Bridget A.; GIETZEN, Kimberly J.
; APPLICANT: XU, Yuming; KALLICK, Deborah A.
; APPLICANT: LEE, Ernestine A.; THANGAVELU, Kavitha
; APPLICANT: DELEGEANE, Angelo M.; LEE, Sally
; TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
; FILE REFERENCE: PP-0794 USN
; CURRENT APPLICATION NUMBER: US/10/312,352
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: PCT/US01/21067
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/ PRIOR FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: US 60/215,454
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 60/219,462
/ PRIOR FILING DATE: 2000-07-18
/ PRIOR APPLICATION NUMBER: US 60/240,111
/ PRIOR FILING DATE: 2000-10-12
/ PRIOR APPLICATION NUMBER: US 60/240,106
/ PRIOR FILING DATE: 2000-10-12
/ PRIOR APPLICATION NUMBER: US 60/244,021
/ PRIOR FILING DATE: 2000-10-27
/ PRIOR APPLICATION NUMBER: US 60/248,887
/ PRIOR FILING DATE: 2000-11-14
/ PRIOR APPLICATION NUMBER: US 60/249,570
/ PRIOR FILING DATE: 2000-11-16
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: PERL Program
/ SEQ ID NO 47
/ LENGTH: 2888
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No. US20040053824A1 184661CB1
US-10-312-352-47

Alignment Scores:
Pred. No.: 2,24e-291 Length: 2888
Score: 2551.00 Matches: 486
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: Gaps: 7

US-10-813-588-2 (1-487) x US-10-312-352-47 (1-2888)

QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB 282 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTTCGGAAGAACAAT 341
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 342 ACAGTACCAAGGGGAAAGACTGATTCAGGTTGGAGATTGGATATCGAATCCAG 401
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
DB 402 ACCTGTGCTTCTGACTATCTCTCTTCCACGACTCTTCAGATCAATATGTCCTACTGT 461
QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
DB 462 GGAAGTATGACTGTTCCCAAGAACTCTTGTGAACACAAAGTGAAGTAACCGTCCGCTTT 521
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 522 GAGAGTGGATCCCACTTCTGCGCGGGTTTTTGTCTGACCTATGGAGACGACCAT 581
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
DB 582 CCAGATTTAATACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA 641
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 642 TTTCTGCCACCTGGTTGTAGACAGTATAGCAGGAGACATTTCTGGGAATATGGTAGATGA 701
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
DB 702 TATAGATATTCCTTTATTTGTGCAAGCTGCCATCCATCGAGGAATATTTCTGATGAA 761
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
DB 762 CTAGGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGATCAGTCGATATGAAGGATTCGT 821
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
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RESULT 12

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US-10-003-132-1
; Sequence 1, Application US/10003132
; Publication No. US20020192750A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Gao, Zeren
; APPLICANT: Shoemaker, Kimberly E.
; TITLE OF INVENTION: NEUROFILIN HOMOLOG 2CUBS
; FILE REFERENCE: 00-62
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DB 822 GCCAATGGTGTCTTTTCGAGGATGGTCCCTGTGACAAAGCGATTCTGTTCCTCC 881
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSer 220
DB 882 AATGGTTGCAGCAGATCCTTGAGTTTGAACCTGACGGCAAAATCAGAGCTTCTTCTCA 941
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 942 TGGCAGTCCGTCAATCAGAGTGGAGACCAAGTTCACTGGTCTCTCTGGCCAGCCGACTT 1001
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 1002 CAGGACCAAGGCCCATCATGGCTTCGGGCGCAGTAGCAACACCAACACACAGAGAG 1061
QY 261 TrpLeuGluIleAspLeuGlyLysLysIleThrGlyIleArgThrGlySer 280
DB 1062 TGGCTGGAGATCGATTTCGGGGAGAAAAGAAAATAACAGGAATTTAGGACCAAGATCT 1121
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
DB 1122 ACACAGTCCAACTTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAACAATAAT 1181
QY 301 SerLysTrpLysThrTyrLysGlyIleValLeuAsnGluGluLysValPheGlnGlyAsn 320
DB 1182 TCTAAGTGGAGACCTATAAGAAATTTGAAATAATGAAGAAAGAGTTTTCAGGGTAAC 1241
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
DB 1242 TCTAACTTTCGGGACCCAGTCGAAACAATTTTCATCCCTCCCATCGTGGCCAGATATGT 1301
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
DB 1302 CGGGTTGTCCCCAGACATGGCCAGAGGATAGCCTTGAAGGTGGAGTCTATTGGTTTC 1361
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
DB 1362 CAGATTACCAAGGTAATGATTTCATTTGGTGGCGCAAGCAAGTCAAGACCAAGTGT 1421
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
DB 1422 TCAACTAAGAAAGAGATGAGACAATCACAGGCCCATCCCTCGGAAGAAACATCCACA 1481
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValLeuValPheAla 420
DB 1482 GGAATAAACAATTACACCGTGGCTATTCCATTGGTGGTCTCTTGTCTGGTGTGTGT 1541
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysGlySerProTyrGlySer 440
DB 1542 GGAATGGGATCTTTTCAGCCCTTTAGAAAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1601
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
DB 1602 GCAGAGCTTCAGAAACACACTGTTGGAAGCAGATTAAATATCCCTTTGCCAGACATCAG 1661
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
DB 1662 TCAGCTGAGTTTACCATCAGCTATGATAATGAAAGGAGATGACACAAAAGTTAGATCTC 1721
QY 481 IleThrSerAspMetAla 486
DB 1722 ATCAACAAGTATATGGCA 1739
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; CURRENT APPLICATION NUMBER: US/10/003,132
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/249,004
; PRIOR FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (76) ... (2223)
US-10-003-132-1

Alignment Scores:

Pred. No.: 2,58e-291 Length: 3151
Score: 2551.00 Matches: 486
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 5 Gaps: 0

US-10-813-588-2 (1-487) x US-10-003-132-1 (1-3151)

```
QY      1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB      232 ATGACATCTAAGATTATCCCGGACCTACCCCATCACACTGTTTGGCAAGACAAAT 291

QY      21 ThrValProLysGlyLysArgLeuLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB      292 ACAGTACCAGGAGGAGAAAGAGATGATTCAGGTTGGGAGATTGGATATCGAATCCAG 351

QY      41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
DB      352 ACCGTGCTTCAGACTATCTCTTCACAGCTCTTCAGATCAATATGGTCCATCTGT 411

QY      61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
DB      412 GGAAGTATGACTGTTCCCAAGACTCTGTTGTAACACAGTGAAGTAACCTCCGCTTT 471

QY      81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB      472 GAGAGTGGATCCACATTTCTGGCGGGGTTTTTGTGACCTATCGAGCAGCAGCCAT 531

QY      101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
DB      532 CCAGATTTAATAACATGTTTGAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA 591

QY      121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB      592 TTCCTGCCAGCTGGTTGTAGACAGCTAGCAGGAGACATTTCTGGGAATATGTTAGATGA 651

QY      141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
DB      652 TATAGAGATACCTCTTTATTTGTCAAAAGCTGCATCCATCCATGAGGAATAATTCCTGATGA 711

QY      161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
DB      712 CTAGGTGGCCAGATCAGTGTCTTACGCCAAGGGATCAGTCGATATGAAGGGATTCTG 771

QY      181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB      772 GCCAATGGTGTCTTTCGAGGATGGTTCCTGTCTGACACAGCGATTCTGTTTACCTCC 831

QY      201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
DB      832 AATGGTTGCAGCAGATCCTTGAGTTTGAACCTGACGGGCAATCAGAGCTTCTTCTCTCA 891

QY      221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB      892 TGGCAGTCGGTCAATGAGAGTGAGACCAAGTTCACTGGTCTCTCTGGCCAGCCCGGACT 951
```

```
QY      241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB      952 CAGGACCAAGGCCCATCATGGCTTCGGGCGACAGTAGCAACACACACACACACAGAG 1011

QY      261 TrpLeuGluIleAspLeuGlyGluLysLysLysIleThrGlyIleArgThrThrGlySer 280
DB      1012 TGGCTGGAGATCGATTTTGGGGGAGAAAAAGAAATAACAGGAATTAGGACCAACAGGATCT 1071

QY      281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
DB      1072 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAACAATAAT 1131

QY      301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
DB      1132 TCTAAGTGGAGACCTATAAAGGAATTTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1191

QY      321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
DB      1192 TCTAACTTTTTCGGGACCCAGTGCAGAAACAATTTTCATCCCTCCATCGTCCGACATATGTG 1251

QY      341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
DB      1252 CGGGTTGTCCCCCAGACATGGCAGGAGTAGCCCTTGAAGGTGGAGCTCAATTGGTTGC 1311

QY      361 GlnIleThrGlnGlnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
DB      1312 CAGATTACACAGGTAAATGATTCATTGGTGTGGCGCAGACAAAGTCAAGACCACTGTT 1371

QY      381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
DB      1372 TCAACTAAGAAAGAGATGAGACAATCAACAGGCCCATCCCTCGGAAGAAACATCCACA 1431

QY      401 GlyIleAsnIleThrValAlaIleProLeuValLeuLeuValValLeuValPheAla 420
DB      1432 GGAATAAACATTACAAACGTTGCTATTCATTGGTGCTCTCTGTGCTCTGGTGTGCT 1491

QY      421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysLysLysLysGln 440
DB      1492 GGAATGGGATCTTTGCAGCCTTTAGAAAGAAAGAAAGAAAGAAAGTCCGTATGATCA 1551

QY      441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
DB      1552 GCAGAGGCTCAGAAACACAGACTGTTTGAAGCAGAGATTAATAATATCCCTTTCCAGACATCAG 1611

QY      461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
DB      1612 TCAGCTGATGTTTACCATCAGCTATGATTAATGAAGAGGAGATGACACAAAGTTAGATCTC 1671

QY      481 IleThrSerAspMetAla 486
DB      1672 ATCACAAGTGATATGGCA 1689
```

RESULT 13

US-09-759-1308-71

; Sequence 71, Application US/097591308

; Publication No. US2003002279A1

; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals, Inc.

; APPLICANT: McCarthy, Sean A

; APPLICANT: Fraser, Christopher C

; APPLICANT: Sharp, John D

; APPLICANT: Barnes, Thomas S

; APPLICANT: Kirt, Susan J

; APPLICANT: Mackay, Charles R

; APPLICANT: Myers, Paul S

; APPLICANT: Leiby, Kevin R

; APPLICANT: Wrighton, Nicolas

; APPLICANT: Goodearl, Andrew

; APPLICANT: Holtzman, Douglas A

; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; USES.
; FILE REFERENCE: MPI00-5350NMIM

/ CURRENT APPLICATION NUMBER: US 09/759,130B
/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: US 09/479,249
/ PRIOR FILING DATE: 2000-01-07
/ PRIOR APPLICATION NUMBER: US 09/559,497
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/578,063
/ PRIOR FILING DATE: 2000-05-24
/ PRIOR APPLICATION NUMBER: US 09/333,159
/ PRIOR FILING DATE: 1999-06-14
/ PRIOR APPLICATION NUMBER: US 09/596,194
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 09/342,364
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: US 09/608,452
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/393,996
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US 09/602,871
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: US 09/420,707
/ PRIOR FILING DATE: 1999-10-19
/ NUMBER OF SEQ ID NOS: 460
/ SOFTWARE: PastSeq for Windows Version 4.0
/ SEQ ID NO 71
/ LENGTH: 3594
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-759-130B-71

Alignment Scores:
Pred. No.: 3,18e-291 Length: 3594
Score: 2551.00 Matches: 486
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 3 Gaps: 0

US-10-813-588-2 (1-487) x US-09-759-130B-71 (1-3594)

QY 1 MetThrSerIleAsnThrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB 228 ATGACATCATTAAGAAATATATCCGGGACCTACCCCAATCACTGTTTGGGAAAGACAAAT 287
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 288 ACAGTACCAAGGGGAAAGACTGATTCTGAGGTTGGGAGATTTGGATATCGAATCCGAG 347
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
DB 348 ACCTGTGCTTCTGACTATCTCTCTTCCAGGCTCTTCAGATCAATATGTTCCATACTGT 407
QY 61 GlySerMetThrValProLysGluLeuLeuLeuLeuLeuLeuLeuLeuLeuValThrValArgPhe 80
DB 408 GGAAGTATGACTGTTCCCAAGAACTCTGTTGGACACAGTGAAGTAACCGTCCGCTTT 467
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 468 GAGAGTGGATCCACATTTCTGCGCGGGTTTTTGTGACCTATCGGAGCAGGACCAT 527
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
DB 528 CCAGATTTAATACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA 587
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 588 TTCTGCCCGACTGTTGTAGACAGCTAGCAGGAGACATTTCTGGGAATATGTTAGATGGA 647
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
DB 648 TATAGAGATACCTCTTTATTGTGCAAGCTGCCATCCATCCAGGAATATGCTGTGAA 707
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180

DB 708 CTAGGTGCCAGATCAGTGTGCTTCAGCGCAAGGATCAGTCGATATGAAGGGATTCTG 767
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB 768 GCCAATGGTGTCTTTCGAGGGATGTTCCCTGTGACACAGCGATTCTGTATTACCTCC 827
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSer 220
DB 828 AATGGTTGCAGCAGATCCTTGAGTTTGAACCTGACGGGCAATCAGAGCTTCTCTCTCA 887
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 888 TGGCAGTCGGTCAATGAGAGTGGACCAAGTTCACTGTCTCTCGGCCCAAGCCGACTT 947
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 948 CAGGACCAAGGCCCATCATGGGCTTCGGGCGAGCAGTAGCAACAACCAACACGAGAG 1007
QY 261 TrpLeuGluIleAspLeuGlyGlyLysLysIleThrGlyIleArgThrThrGlySer 280
DB 1008 TGGCTGGAGATCGATTTGGGGGAGAAAAATAACAGGAATTAGGACCAAGATCT 1067
QY 281 ThrGlnSerAsnAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
DB 1068 ACAGATCGAATCTCAACTTTTATGTTAAGAGTTTGTGATGAATTTCAAAACAATAAT 1127
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGlyLysValPheGlnGlyAsn 320
DB 1128 TCTAAGTGAAGACCTATAAAGGAATTTGTAATATGAAGAAAGGTGTTTCAGGGTAAC 1187
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
DB 1188 TCTAATCTTTCGGGACCCAGTGCACAAACAATTTTCATCCCTCCATCGTGGCCAGATATGT 1247
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLeuValGluLeuIleGlyCys 360
DB 1248 CGGGTTGTCCCCCAGACATGGCAGAGGATAGGCTTGAAGGTGAGCTCATTTGGTTGC 1307
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
DB 1308 CAGATTACACAGGTAATGATTTCATTGTTGTCGCGCAAGACAAGTCAAAAGCACCAGTGT 1367
QY 381 SerThrLysGlyGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
DB 1368 TCAACTTAAGAAAGAGATGAGACAATCACAAGGCCCATCCCTCGGAAGAAACATCCACA 1427
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValPheAla 420
DB 1428 GGAATAAACATTACACGGTGGCTATTTCCATTGGTGCTCTTGTGTTCTCTGTGTTGCT 1487
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysLysLysLysLys 440
DB 1488 GGAATGGGATCTTTGCAGCCTTTAGAAAGAAAGAAAGAAAGAAAGTCCGTATGATCA 1547
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
DB 1548 GCAGAGGCTCAGAAAAACAGACTGTTGGAAGCAGATTAAATATATATATATATATATAT 1607
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLysLeu 480
DB 1608 TCAGCTGAGTTTACCATCATGCTATGATATATGAGAGGAGATGACACAAAAGTTAGATCTC 1667
QY 481 IleThrSerAspMetAla 486
DB 1668 ATCACAAGTGAATGCA 1685

RESULT 14

US-10-741-790-71
; Sequence 71, Application US/10741790
; Publication No. US20040121396A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: McCarthy, Sean A
APPLICANT: Fraser, Christopher C
APPLICANT: Sharp, John D
APPLICANT: Barnes, Thomas S
APPLICANT: Kirst, Susan J
APPLICANT: Mackay, Charles R
APPLICANT: Myers, Paul S
APPLICANT: Leiby, Kevin R
APPLICANT: Wrighton, Nicolas
APPLICANT: Goodearl, Andrew
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES
FILE REFERENCE: MPI00-5350NMIM
CURRENT APPLICATION NUMBER: US/10/741,790
PRIOR FILING DATE: 2003-12-19
PRIOR APPLICATION NUMBER: US 09/479,249
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/608,452
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/393,996
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 71
LENGTH: 3594
TYPE: DNA
ORGANISM: Homo sapiens
US-10-741-790-71

Alignment Scores:
Pred. No.: 3,18e-291 Length: 3594
Score: 2551.00 Matches: 486
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 7 Gaps: 0

US-10-813-588-2 (1-487) x US-10-741-790-71 (1-3594)

Qy 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
Db 228 ATGACATCTAAGAAATTATCCCGGACCTACCCCAATCACACTGTTTGGAAAGACAAATT 287

Qy 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
Db 288 ACAGTACCAAGGGGAAAGACTGATTCTGAGGTTGGGAGATTTCGATATCGAATCCCAAG 347

Qy 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
Db 348 ACCCTGTCTTCGACTATCTCTCTCCACCACTCTTCAGATCAATATGATGCTCACTACTGT 407

Qy 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
Db 408 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTGACACAGTGAAGTAACTGCTCGCTTT 467

Qy 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
Db 1548 GCAGAGGCTCAGAAACAGACTGTTGGAAGCAGAGATTAATAATATCCCTTTGCCAGACATCAG 1607

Db 468 GAGAGTGGATCCACATTTCTGGCCGGGGTTTTTTTGTCTGACCTATTCGAGCAGCGACCAT 527
Qy 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrTyrLeuLysThrGluTyrSerLys 120
Db 528 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCCATATTATTGAAGACAGATACACAAA 587
Qy 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
Db 588 TTCTGCCAGCTGGTTGTAGACAGCTAGCAGAGACATTTCTGGGAATATGTTAGATGGA 647
Qy 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
Db 648 TATAGAGATACCTCTTTATTGTGCAAGCTGCATCATCTGAGGAATAATTGCTGATGAA 707
Qy 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
Db 708 CTAGGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATCAAGGGATTCTG 767
Qy 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
Db 768 GCCAATGGTGTCTTTTCAGGGGATGGTTCCTGTGTCAGACACAGCGATTTCTGTTACTCC 827
Qy 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
Db 828 AATGGTTGCAGCAGATCCTTGAGTTTGAACCTGACGGGCAAAATCAGAGCTTCTTCTCA 887
Qy 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
Db 888 TGGCAGTGGTCAATGAGAGTGGAGACCAAGTTCACTGGTCTCTCTGGCCCAAGCCCACTT 947
Qy 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
Db 948 CAGGACCAAGGCCCATCATGGCTTCGGGGGACAGTACGACACACACCAACACGAGAG 1007
Qy 261 TrpLeuGluIleAspLeuGlyLysLysIleThrGlyIleArgThrThrGlySer 280
Db 1008 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACACACAGGATCT 1067
Qy 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
Db 1068 ACACAGTCGAATCTCAACTTTTATGTTAAGAGTTTGTGATGAATTTCAAAACCAATAAT 1127
Qy 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn 320
Db 1128 TCTAAGTGGAGACCTATTAAGGAATTTGTAATATGAAGAAAGAGTGTTCAGGGTAAC 1187
Qy 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
Db 1188 TCTAACTTTTCGGGACCCAGTGCACAAACAAATTTTCATCTCCCTCCATCGTGGCCAGATATG 1247
Qy 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
Db 1248 CGGGTTGTCCCCCAGACATGGCACCAGAGGATAGCTTTGAAGGTGGAGCTCAATGGTTGC 1307
Qy 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
Db 1308 CAGATTACACAGGTAAATGATTCTTGTGTGGCCCAAGACAGTCAAGTCAAGACACAGTGT 1367
Qy 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
Db 1368 TCAACTAAGAAGAAGATGAGACAAATCAAGGCCCATCCCTCCGGAAGAAACATCCACA 1427
Qy 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValIleValPheAla 420
Db 1428 GGAATAAACAATTACAAACGGTGGCTATTCCATTGGTGGCTCTTGTGTTGCTGTGTGCT 1487
Qy 421 GlyMetGlyIlePheAlaPheArgLysLysLysLysLysLysLysLysLysLysLys 440
Db 1488 GGAATGGGATCTTTGACAGCTTTAGAAAGAAGAGAGAGAGAGAGAGTCCGTATGATCA 1547
Qy 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
Db 1548 GCAGAGGCTCAGAAACAGACTGTTGGAAGCAGAGATTAATAATATCCCTTTGCCAGACATCAG 1607

QY 461 SerAlaGluPheThrIleSerTyrAspAenGluLysGluMetThrGlnLysLeuAspLeu 480
Db 1608 TCAGCTGAGTTTACCATCAGCTATGATAATGAGAGGAGATGACACAAAAGTTAGATCTC 1667

QY 481 IleThrSerAspMetAla 486
Db 1668 ATCACAAGTGATATGGCA 1685

RESULT 15

US-09-814-353-20367
Sequence 20367, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037

SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 20367
LENGTH: 3676
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3676
OTHER INFORMATION: n = A,T,C or G
US-09-814-353-20367

Alignment Scores:
Pred. No.: 3,29e-291 Length: 3676
Score: 2551.00 Matches: 486
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 3 Gaps: 0

US-10-813-588-2 (1-487) x US-09-814-353-20367 (1-3676)

QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
Db 294 ATGACATCTAAGAAATATCCCGGAGCTACCCCAATCACACTGTTTGGGAAAGACAAAT 353
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
Db 354 ACAGTACCAAGGGGAAAGACTGTTCTGAGGTTGGGAGATTTGGATATCGAATCCCGAG 413
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
Db 414 ACCTGTGCTTCTGACTATCTTCTTCCACGAGCTCTTCAGATCAATATGTCCTACTGT 473
QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
Db 474 GGAAGTATGACTGTTCACCAAGAAGACTCTTGTGTGAACACAAAGTGAAGTAAACCGTCGCTTT 533

QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerSerHis 100
Db 534 GAGAGTGGATCCACATTTCTGGCCGGGGTTTTTGTCTGACCATATCGAGAGCGACCAT 593
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
Db 594 CCAGATTATTAACATGTTTGGACGAGCTAGCCATTTATTTGAAGACAGATACAGCAAA 553
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
Db 654 TTCTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGTGTAGTGA 713
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
Db 714 TATAGAGATACCTCTTTATTTGCAAGAGCTGCATCCATTCAGAGGAATATTTCTGTATGA 773
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
Db 774 CTAGGTGGCCAGATCAGTGTGCTTCAGCCAAAGGATCAGTCGATATGAGGGATCTTG 833
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
Db 834 GCCAATGGTGTCTTTTCGAGGGATGGTTCCCTGTGCAGCAAGCGATTTCTGTTCCTCC 893
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
Db 894 AATGGTTGCAGCAGATCCTTTGAGTCTTGAACCTGACGGGCAATTCAGAGCTTCTTCTCA 953
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
Db 954 TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTTCACTGTCTCTGGCCAGCCGACTT 1013
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
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QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValLeuValPheAla 420
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Perfect score: 1464
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 588141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

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Listing first 45 summaries

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- 1: gb_ba.*
- 2: gb_in.*
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- 8: gb_pr.*
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- 10: gb_sts.*
- 11: gb_sy.*
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- 13: gb_vi.*
- 14: gb_htg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1464	100.0	1464	6 AR542471	Sequence
2	1464	100.0	1464	6 AX118816	Sequence
3	1464	100.0	1620	6 AR542473	Sequence
4	1464	100.0	1620	6 AX118820	Sequence
5	1464	100.0	1761	6 AR542472	Sequence
6	1464	100.0	1761	6 AX118818	Sequence
7	1464	100.0	1768	6 AR542474	Sequence
8	1464	100.0	1768	6 AX118822	Sequence
9	1462.4	99.9	2010	6 CQ870614	Sequence
10	1462.4	99.9	2010	6 CQ870615	Sequence
11	1462.4	99.9	2010	8 BC035671	Sequence
12	1459.8	99.7	2888	6 AX704743	Sequence
13	1459.8	99.7	3676	6 CO413296	Sequence
14	1440.2	98.4	2547	6 AX833875	Sequence
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28	219.4	15.0	407	8 BD059592	Secrete
29	218	14.9	100808	8 HS94G16	Human DNA s
30	218	14.9	178670	14 AC138943	Homo sapi
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45	204	13.9	2280	6 AX615194	Sequence

ALIGNMENTS

RESULT 1
AR542471
LOCUS AR542471 1464 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 1 from patent US 6743907.
ACCESSION AR542471
VERSION AR542471.1 GI:53934937
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1464)
AUTHORS Donoho G., Turner, C.A. Jr., Nehls, M.C., Friedrich, G., Zambrowicz, B. and Sands, A.T.
TITLE Human proteins and polynucleotides encoding the same
JOURNAL Patent: US 6743907-A 1 01-JUN-2004;
LEXICON Lexicon Genetics Incorporated; The Woodlands, TX
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Db	181	GGAAATGATGACTGTTTCCCAAGAACTCTTGTGTAACA	CAAGTGA	AGTACCG	TCGCTTT 240

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AX118816 1464 bp DNA linear PAT 11-MAY-2001
LOCUS Sequence 1 from Patent WO0129219.
ACCESSION AX118816
VERSION AX118816.1 GI:14035774
KEYWORDS Homo sapiens (human)
SOURCE .
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1
AUTHORS Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and
Sandes, A.T.
TITLE Human cub-domain-containing protein and gene encoding the same
JOURNAL Patent: WO 0129219-A 1 26-APR-2001;
Lexicon Genetics Incorporated (US)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AR542473
LOCUS

Sequence 5 from patent US 6743907.
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REFERENCE
AUTHORS
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RESULT 4
AX118820
LOCUS AX118820 1620 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 5 from Patent WO0129219.
ACCESSION AX118820
VERSION AX118820.1 GI:14035776
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and
Sands, A.T.
Human cub-domain-containing protein and gene encoding the same
Patent: WO 0129219-A 5 26-APR-2001;
Lexicon Genetics Incorporated (US)
FEATURES
Location/Qualifiers
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source
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Best Local Similarity 100.0%; Pred. No. 0;
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AUTHORS	Donoho,G., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B. and Sands,A.T.			Db	1258	TCTAAGTGGAGACCTATAAAGGAATTTGTAATAATGAAGAAAAAGGTGTTTCAGGGTAAC	1317
TITLE	Human proteins and polynucleotides encoding the same			QY	1021	CGGGTGTCCCCAGACATGGCACAGAGGATAGCTTTGAAGTGGAGCTCATTTGGTTGC	1080
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KEYWORDS
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ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE
AUTHORS Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and
Sands, A.T.
TITLE Human cub-domain-containing protein and gene encoding the same
JOURNAL Patent: WO 0129219-A 3 26-APR-2001;
Lexicon Genetics Incorporated (US)
FEATURES
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DEFINITION Sequence 23 from Patent WO2004073657.
ACCESSION CQ870614
VERSION CQ870614.1 GI:52000125
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Aziz,N., Gish,K.C., Wilson,K.E. and Zlotnik,A.
TITLE Methods of diagnosis of cancer, composition and methods of
screening for modulators of cancer
JOURNAL Patent: WO 2004073657-A 23 02-SEP-2004;
PROTEIN DESIGN LABS, INC. (US)
FEATURES
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ORIGIN

Query Match 99.9%; Score 1462.4; DB 6; Length 2010;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION Sequence 24 from Patent WO2004073657.
ACCESSION CQ870615
VERSION CQ870615.1 GI:52000126
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1
AUTHORS Aziz,N., Gish,K.C., Wilson,K.E. and Zlotnik,A.
TITLE Methods of diagnosis of cancer, composition and methods of
screening for modulators of cancer
JOURNAL Patent: WO 2004073657-A 24 02-SEP-2004;
PROTEIN DESIGN LABS, INC. (US)
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"

ORIGIN

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1441 ATCACAAAGTGATGATGCAGGTTAA 1464
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Db 1722 ATCACAAAGTGATGATGCAGGTTAA 1745

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BC035671
LOCUS 2010 bp mRNA linear PRI 25-JUL-2005
DEFINITION Homo sapiens discoidin, CUB and LCCL domain containing 1, mRNA
(cDNA clone MGC:46341 IMAGE:5730536), complete cds.

ACCESSION BC035671
VERSION 1
KEYWORDS GI:23274238
SOURCE MGC.

ORGANISM Homo sapiens (human)
Homo sapiens

REFERENCE 1 (bases 1 to 2010)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haie, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Loquellano, N.A., Peters, G.J.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, K.D., Mullah, J.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

REFERENCE 2 (bases 1 to 2010)
AUTHORS NIH MGC Project

Direct Submission
Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-x@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Hagnigh, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

CONSTRM
TITLE Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL 12477932
PUBMED 2 (bases 1 to 2010)

REFERENCE 2 (bases 1 to 2010)
AUTHORS NIH MGC Project

Direct Submission
Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-x@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Hagnigh, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

REMARK
COMMENT

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 79 Row: i Column: 21
This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 27735142.

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ORIGIN

Query Match 99.9%; Score 1462.4; DB 8; Length 2010;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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AX704743
Version
AX704743.1
GI:29561409
Keywords
AX704743
Sequence 47 from Patent WO0202634.
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Linear
PAT 04-APR-2003

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AUTHORS	Gururajan, R., Hafalia, A.J., Kallick, D.A., Patterson, C., Azimzai, Y., Khan, F.A., Xu, Y., Yao, M.G., Yue, H., Au-Young, J., Batra, S., Baughn, M.R., Borowsky, E.A., Lo, T.P., Lu, D.A., Lu, Y., Tang, Y.T., Yang, J., Zingler, K.A., Deleage, A.M., Gietzen, K., Marcus, G.A., Nguyen, D.B., Policky, J.L., Ramkumar, J., Thangavelu, K., Wallia, N.K. and Warren, B.A.	Db	1062	TGGCTGGAGATCGATTTGGGGGAGAAAAAATAACAGGAATTAAGGACCAAGATCT	1121
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DEFINITION	CO413296				
ACCESSION	CO413296.1				
VERSION	GI:41321077				
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SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Lee, J. and Lillie, J.				
TITLE	Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer				
JOURNAL	Patent: WO 0170979-A 20367 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)				

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Best Local Similarity 99.9%; Pred. No. 0;			
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DB	354	ACAGTACCAGGAGGAAAGACATGATTCAGGTGCGGAGAT	TTGGATATCGGAATCCCGAG 413
QY	121	ACCTGTGCTTCTGACTATCTTCTTCCACGAGCTCTTCAG	ATCAATATGCTCCATCTGT 180
DB	414	ACCTGTGCTTCTGACTATCTTCTTCCACGAGCTCTTCAG	ATCAATATGCTCCATCTGT 473
QY	181	GGAAGTATGACTGTTCCCAAGAACTCTTGTGGAACA	CAAGTGAAGTAAACCGTCCGCTTT 240
DB	474	GGAAGTATGACTGTTCCCAAGAACTCTTGTGGAACA	CAAGTGAAGTAAACCGTCCGCTTT 533
QY	241	GAGAGTGGATCCCACTATTTCTGCGCGGGTTTTTCTG	CTACCTATCGGAGCAGCAAT 300
DB	534	GAGAGTGGATCCCACTATTTCTGCGCGGGTTTTTCTG	CTACCTATCGGAGCAGCAAT 593
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Sequence 999 from Patent EP1347046.			
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VERSION			
AX833875.1 GI:39920010			
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ORGANISM			
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Hominidae; Homo.			
REFERENCE			
AUTHORS			
Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and Masuho, Y.			
TITLE			
Full-length cDNA sequences			
JOURNAL			
Patent: EP 1347046-A 999 24-SEP-2003;			
Research Association for Biotechnology (JP)			
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AK095973 GI:21755342
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Homo sapiens (human)
Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1
Oca.T., Suzuki.Y., Nishikawa.T., Otsuki.T., Sugiyama.T., Irie.R., Wakamatsu.A., Hayashi.K., Sato.H., Nagai.K., Kimura.K., Makita.H., Sekine.M., Obayashi.M., Nishi.T., Shibahara.T., Tanaka.T., Ishii.S., Yamanoto.J., Saito.K., Kawai.Y., Isono.Y., Nakamura.Y., Nagahara.K., Murakami.K., Yasuda.T., Iwayanagi.T., Wagatsuma.M., Shiratori.A., Sudo.H., Hosoiri.T., Kaku.Y., Kodaira.H., Kondo.H., Sugawara.M., Takahashi.M., Kanda.K., Yokoi.T., Furuya.T., Kikkawa.E., Omura.Y., Abe.K., Kamihara.K., Katsuta.N., Sato.K., Tanikawa.M., Yamazaki.M., Ninomiya.K., Ishibashi.T., Yamashita.H., Murakawa.K., Fujimori.K., Tanai.H., Kimata.M., Watanabe.M., Hiraoka.S., Chiba.Y., Ishida.S., Ono.Y., Takiguchi.S., Watanabe.S., Yosida.M., Hotuta.T., Kusano.J., Kanehori.K., Takahashi-Fujii.A., Hara.H., Tanase.T., Nomura.Y., Togiya.S., Komai.F., Hara.R., Takeuchi.K., Arita.M., Imose.N., Musashino.K., Yuuki.H., Oshima.A., Sasaki.N., Aotaka.S., Yoshikawa.Y., Matsunawa.H., Ichihara.T., Sashihata.N., Sano.S., Moriya.S., Momiyama.H., Satoh.N., Takami.S., Terashima.Y., Suzuki.O., Nakagawa.S., Senoh.A., Mizoguchi.H., Goto.Y., Shimizu.F., Wakebe.H., Hishigaki.H., Watanabe.T., Ozaki.K., Hirao.M., Ohmori.Y., Kawabata.A., Hikiji.T., Kobatake.N., Inagaki.H., Ikema.Y., Okamoto.S., Okitani.R., Kawakami.T., Noguchi.S., Itoh.T., Shigetake.K., Senba.T., Macsumura.K., Oyama.M., Mizuno.T., Morinaga.M., Sasaki.M., Togashi.T., Oyama.H., Watanabe.M., Komatsu.T., Mizushima-Sugano.J., Satoh.T., Shirai.Y., Takahashi.Y., Nakagawa.K., Okumura.K., Nagase.T., Nomura.N., Kikuchi.H., Masuho.Y., Yamashita.R., Nakai.K., Yada.T., Nakamura.Y., Ohara.O., Isogai.T. and Sugano.S.
Complete sequencing and characterization of 21,243 full-length human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
14702039
JOURNAL
PUBMED
REFERENCE

AUTHORS

Nishi, T., Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshina, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
Unpublished

TITLE

3 (bases 1 to 2547)

REFERENCE

Isogai, T. and Yamamoto, J.

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

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ORIGIN

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DB 205 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACACTGTTTGGCGAAAGACAAT 264
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DB 385 GGAAGTATGACTGTTTCCCAAGAACTCTTGTGGAACAAGTGAAGTAAACCGTCCGCTTT 444
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DB 445 GAGAGTGGATCCCAATTTCTGGCGGGGGTTTTTGTGCTACCTATGCGAGCAGCCAT 504
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Qy 1441 ATCACAAGTGATATGGCAGGTTA 1463
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Db 1641 ATCACAAGTGATATGGCAGGTTA 1663
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Search completed: January 15, 2006, 17:51:25
Job time : 7275 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2006, 19:46:38 ; Search time 250 Seconds
(without alignments)
3462.690 Million cell updates/sec

Title: US-10-813-588-2

Perfect score: 2557

Sequence: 1 MTSKNVPGTYPNHTVCKETI.....YDNKEKMTQKLDLITSDMAG 487

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2557	100.0	1620	3	US-09-691-344A-5
3	2557	100.0	1761	3	US-09-691-344A-3
4	2557	100.0	1768	3	US-09-691-344A-7
5	1146.5	44.8	1871	3	US-09-823-038A-43
6	867.5	33.9	2310	3	US-10-191-436A-7
7	867.5	33.9	2310	3	US-10-191-436A-9
8	860.5	33.7	2328	3	US-10-191-436A-1
9	860.5	33.7	2328	3	US-10-191-436A-3

10	856.5	33.5	2310	3	US-10-191-436A-4	Sequence 4, Appli
11	856.5	33.5	2310	3	US-10-191-436A-6	Sequence 6, Appli
12	331.5	13.0	3371	3	US-09-116-473-1	Sequence 1, Appli
13	329.5	12.9	2730	3	US-08-936-135-17	Sequence 17, Appli
14	329.5	12.9	2730	3	US-09-439-711C-17	Sequence 17, Appli
15	329.5	12.9	2781	3	US-08-936-135-19	Sequence 19, Appli
16	329.5	12.9	2781	3	US-09-439-711C-19	Sequence 19, Appli
17	329.5	12.9	3404	3	US-09-583-638-3	Sequence 3, Appli
18	324.5	12.7	3539	3	US-08-936-135-7	Sequence 7, Appli
19	324.5	12.7	3539	3	US-09-439-711C-7	Sequence 7, Appli
20	324.5	12.7	4718	3	US-08-936-135-9	Sequence 9, Appli
21	324.5	12.7	4718	3	US-09-439-711C-9	Sequence 9, Appli
22	324.5	12.7	4733	3	US-08-936-135-11	Sequence 11, Appli
23	324.5	12.7	4733	3	US-09-439-711C-11	Sequence 11, Appli
24	324.5	12.7	4765	3	US-08-936-135-21	Sequence 21, Appli
25	324.5	12.7	4765	3	US-09-439-711C-21	Sequence 21, Appli
26	324.5	12.7	4769	3	US-08-936-135-13	Sequence 13, Appli
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28	324.5	12.7	4780	3	US-08-936-135-23	Sequence 23, Appli
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33	321	12.6	6914	3	US-09-949-002-6	Sequence 6, Appli
34	321	12.6	6987	3	US-09-949-002-231	Sequence 231, App
35	318	12.4	6585	3	US-08-746-111-4	Sequence 4, Appli
36	317	12.4	6509	2	US-08-804-196-1	Sequence 1, Appli
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38	317	12.4	6509	3	US-08-746-111-26	Sequence 26, Appli
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ALIGNMENTS

RESULT 1

US-09-691-344A-1
; Sequence 1, Application US/09691344A
; Patent No. 6743907
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6743907el Human Proteins and Polynucleotides
; FILE REFERENCE: LEX-0071-USA
; CURRENT APPLICATION NUMBER: US/09/691,344A
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/183,583
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-691-344A-1

Alignment Scores: 1.35e-279 Length: 1464
Pred. No.: 2557.00 Matches: 487
Score: 100.00%
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0

Query Match:	100.00%	Indels:	0
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QY	1	MetThrSerIysAsnTyrProGlyThrTyrProAsnHisThrValCysGluIysThrIle	20
DB	1	ATGACATCTAAGAAATATATCCCGGACCTACCCCAATCACACTGTTTTCGGAAAGACAAAT	60
QY	21	ThrValProIysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln	40
DB	61	ACAGTACCAAGGGGAAAGACTGATCTCAGGTTGGAGATTGGATATCGAATCCAG	120
QY	41	ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys	60
DB	121	ACCTGTGCTTCTGACTATCTCTCTTCCAGGCTCTTCAGATCAATATGTCATACTGT	180
QY	61	GlySerMetThrValProIysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe	80
DB	181	GGAAGTATGACTGTTCCCAAGAACTCTTGTTGAAACAAAGTGAAGTAACCGTCCGCTTT	240
QY	81	GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis	100
DB	241	GAGAGTGGATCCCAATTTCTGCGCGGGTTTCTGCTGACCTATGCGAGCAGCCAT	300
QY	101	ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuIysThrGluTyrSerLys	120
DB	301	CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTTATTGGAAGCAGAAATACAGCAA	360
QY	121	PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly	140
DB	361	TTCTGCCACGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTCGGAATATGGTAGATGA	420
QY	141	TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleLeuAlaAspGlu	160
DB	421	TATAGAGATACCTCTTTATTGTGCAAGCTGCCATCCATGACAGGAATATGCTGATGA	480
QY	161	LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu	180
DB	481	CTAGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATGATGAAGGATCTG	540
QY	181	AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer	200
DB	541	GCCAAATGGTGTCTTTCAGAGGATGGTTCCTCTGCAGCAAGGATTTCTGTTACCTCC	600
QY	201	AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer	220
DB	601	AATGGTTGCAGCAGATCTTGAGTTTGAACCTGACGGCAATCAGAGCTTCTTCTCA	660
QY	221	TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu	240
DB	661	TGGCAGTCGGTCAATGAGAGTGGAGCAAGTTCACTGGTCTCTCTGCGCAAGCCGACTT	720
QY	241	GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnHisLysProArgGlu	260
DB	721	CAGACCAAGGCCCATCATGGGCTTCGGCGACAGTAGCAACCAACCAACCCAGAG	780
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DB	781	TGGCTGGAGATCGATTTGGGGGAGAAAGAAATACAGGAATTAGGACCAAGGATCT	840
QY	281	ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn	300
DB	841	ACACAGTCGAACCTCAACTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAAACAATA	900
QY	301	SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn	320
DB	901	TCTAAGTGGAGACCTTAAGAGGAATTTGTAATAATGAAGAAAGGTTTTCAGGGTAAC	960
QY	321	SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal	340
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QY	361	GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal	380
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QY	401	GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValLeuValPheAla	420
DB	1201	GGAAATAAACATTTACACGGTGGCTATTCCATTGGTGTCTCTTGTCTCTGGTGTGTCT	1260
QY	421	GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysLysLysLysLys	440
DB	1261	GGATGGGATCTTTTGCAGCCTTTAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1320
QY	441	AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln	460
DB	1321	CGGAGGCTCAGAAAACAGACTGTTTGAAGCAGATTAAATATCCCTTTGCCAGACATCAG	1380
QY	461	SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu	480
DB	1381	TCAGCTGAGTTCACCATCAGCTATGATAATGAAGAGAGATGACACAAAAGTTTAGATCTC	1440
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; Sequence 5, Application US/09691344A			
; Patent No. 6743907			
; GENERAL INFORMATION:			
; APPLICANT: Donoho, Gregory			
; APPLICANT: Turner, C. Alexander Jr.			
; APPLICANT: Nehls, Michael			
; APPLICANT: Friedrich, Glenn			
; APPLICANT: Zambowicz, Brian			
; APPLICANT: Sands, Arthur T.			
; TITLE OF INVENTION: No. 6743907el Human Proteins and Polynucleotides			
; TITLE OF INVENTION: Encoding the Same			
; FILE REFERENCE: LEX-0071-USA			
; CURRENT APPLICATION NUMBER: US/09/691,344A			
; CURRENT FILING DATE: 2000-10-18			
; PRIOR APPLICATION NUMBER: US 60/160,285			
; PRIOR FILING DATE: 1999-10-19			
; PRIOR APPLICATION NUMBER: US 60/183,583			
; PRIOR FILING DATE: 2000-02-18			
; NUMBER OF SEQ ID NOS: 7			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 5			
; LENGTH: 1620			
; TYPE: DNA			
; ORGANISM: homo sapiens			
US-09-691-344A-5			
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Score:	2557.00	Matches:	487
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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
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QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
DB 457 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTGAAGACAGAAATACAGCAAA 516
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QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
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DB 817 TGGCAGTCCGTCAATGAGAGTGGAGACCAAGTTCACTGTCTCTCTGGCCAAAGCCGACTT 876
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 877 CAGGACCAAGGCCCATCATGGGCTTGGGGCGACAGTAGCAACCAACCAACCAACGAGAG 936
QY 261 TrpLeuGluIleAspLeuGlyLysLysIleThrGlyIleArgThrThrGlySer 280
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QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
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DB 1177 CGGGTGTGCCCCAGACATGGCACCAGAGCATAGCTTGAAGGTGGAGCTCATTTGGTTGC 1236
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DB 1357 GGAATAAAACATTTACAACGGTGGCTATTCATTGGTGGTCTCTTGTGCTCTGGTGTGCT 1416
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DB 1477 GCGGAGGCTCAGAAACAGACTGTTGGAAGCAGATTAATATATCCCTTTGCCAGACATCAG 1536
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DB 1537 TCAGCTGAGTTTACCATTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1596
QY 481 IleThrSerAspMetAlaGly 487
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; Sequence 3, Application US/09691344A
; Patent No. 6743907
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6743907el Human Proteins and Polynucleotides
; FILE REFERENCE: LEX-0071-USA
; CURRENT APPLICATION NUMBER: US/09/691,344A
; PRIOR FILING DATE: 2000-10-18
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-691-344A-3
Alignment Scores:
Pred. No.: 1,856-279 Length: 1761
Score: 2557.00 Matches: 487
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-813-588-2 (1-487) x US-09-691-344A-3 (1-1761)
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DB 298 ATGACATCTTAAGAAATTATCCCGGACCTACCCCAATCACACTGTTTGGGAAAGACAAT 357
QY 21 ThrValProLysGlyLysArgLeuLeuLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 358 ACAGTACCAAGGGGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCCAAG 417
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
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141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
Db TATAGAGATACCTTCTTATTTGTGCAAGCTGCCATCCATCGAGAATAATTTGTGTAGAA 538
161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
Db CTAGGTGGCCAGATCATGTGCTTCAGCGCAAGGGATCAGTCGATGAGGGATCTG 598
181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
Db GCCAATGGTGTCTTTTCGAGGATGGTTCCCTGCAGACAAGCGATTTCTGTTTACCTCC 658
201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
Db AATGGTTCAGCAGATCCCTTGAGTTTGAACCTGACGGGCAAAATCAGAGCTTCTTCTCA 718
221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
Db TGGCAGTCGGTCAATGAGAGTGAGACCAAGTTCATCTGCTCTCGCCAGCCCACTT 778
241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
Db CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACAACCAACCAACCCAGAG 838
261 TrpLeuGluIleAspLeuGlyLysLysLysLysIleThrGlyIleArgThrGlySer 280
Db TGGCTGGAGATCGATTGGGGGAGAAAAAGAAATTAACAGGAATTAGGACCAAGATCT 898
281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
Db ACACAGTCGACTTCACTTTTATGTTAGAGTTTGTGATGACTTCAAAACAATAAT 958
301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
Db TCTAAGTGAAGACCTATAAGGAATTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1018
321 SerAsnPheArgAspProValGlnAsnAsnPheIleProIleValAlaArgTyrVal 340
Db TCTAAGTTCGGGACCCAGTGCAGAAACAATTTTCATCCCTCCATCGTGGCCAGATATGT 1078
341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
Db CGGGTGTCCCCAGACATGGCCAGAGATAGCCCTTGAAGTGGAGCTCATTTGGTTGC 1138
361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
Db CAGATTACACAAGGTAATGATTTCATTTGGTGGCGCAAGCAAGTCAAGACCAAGTGT 1198
381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
Db TCAACTTAAGAAAGAGATGAGACAATCAAGAAGCCCATCCCTCGGAAGAAACATCCACA 1258
401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValLeuValPheAla 420
Db GGNATHAACATTACACGGTGGCTATTCATTGGTCTCTCTGTTGCTGGTGTGTGT 1318
421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysGlySerProTyrGlySer 440
Db GGAATGGGATCTTTTCAGCCCTTTAGAAAGAGAGAGAGAGAGAGAGTCCGTATGATCA 1378
441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
Db GCGGAGGCTCAGAAAAACAGACTGTTGGAAGCAGATTAATAATATCCCTTTGCCAGACATCAG 1438

461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
Db TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAAGTTAGATCTC 1498
481 IleThrSerAspMetAlaGly 487
Db ATCACAAGTGATATGGCAGGT 1519
RESULT 5
US-09-823-038A-43
; Sequence 43, Application US/09823038A
; Patent No. 6797271
; GENERAL INFORMATION:
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Abernethy, Nevin
; APPLICANT: Onrust, Rene
; APPLICANT: Kumble, Anand
; APPLICANT: Murison, Greg
; TITLE OF INVENTION: Compositions Isolated From Stromal Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1037c3
; CURRENT APPLICATION NUMBER: US/09/823,038A
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 1871
; TYPE: DNA
; ORGANISM: Mouse
US-09-823-038A-43
Alignment Scores:
Pred. No.: 1,96e-119 Length: 1871
Score: 1146.50 Matches: 236
Percent Similarity: 53.50% Conservative: 24
Best Local Similarity: 48.56% Mismatches: 27
Query Match: 44.84% Indels: 199
Db: 3 Gaps: 1
US-10-813-588-2 (1-487) x US-09-823-038A-43 (1-1871)
QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
Db 193 ATGACATCTAAGATATATCCAGGACTTACCCCATTTACACHTGTGTGAAAGATCATC 252
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
Db 253 ACAGTCCCAAGGGGAAGAGACTTATCTGAGGTTGGGAGATTTGAACATTGAGTCCAAG 312
QY 41 ThrCysAlaSerAspTyrIleLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
Db 313 ACCTGGCTTCTGACTATCTCTTCAGCAGTGCAGATCAGATGATGTCATATGTTGT 372
QY 61 GlySerMetThrValProLysGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
Db 373 GGGAGTGGGTGTTTCCCAAGAACTCCGGCTGAACTCAACAGAGTGTACTGTCTCTTC 432
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuLeuLeuLeuLeuLeuLeuLeu 100
Db 433 AAGAGTGGATCTCACATTTCTGGCGGGGCTTCTGCTGACCTACGCCAGCAGTGCACAT 492
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
Db 493 CCAGATTTAATAACCTGTTTGGAGAGGAGCCCATTTATTCGAGGAAAAATACAGCAA 552
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
Db 553 TTCTGCCAGCTGGCTGTAGACATAGCAGAGATATTTCTGGGGAATACAAAAGATGTT 612
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
Db 613 TACAGAGATACCTCTTTTATTTGTGCAAGCTGCCATCCAGCGGAGATCATCACAGATGAA 672

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QY 161 LeuGlyGlyClnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
Db 673 CTAGGTGGCCACATCACTGCTTCAGACAAAGGATAAGTCACTATGAAGACTCCGTG 732
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
Db 733 GCCAATGGGTGCTCTCCCGCATGTTCTTTCGGAAGAGGATTCCTTTT 786
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyClnIleArgAlaSerSer 220
Db 786 ----- 786
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
Db 786 ----- 786
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
Db 786 ----- 786
QY 261 TrpLeuGluIleAspLeuGlyGluLysLysIleThrGlyIleArgThrThrGlySer 280
Db 786 ----- 786
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPhelLysAsnAsn 300
Db 786 ----- 786
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
Db 786 ----- 786
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProIleValAlaArgTyrVal 340
Db 786 ----- 786
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
Db 786 ----- 786
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
Db 786 ----- 786
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
Db 787 -----ACACCCCA 795
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValLeuValPheAla 420
Db 796 GGAATGAATATTACAATGTGGCGATTCCCATGATGATCTCATCGCCCTCTCTGACT 855
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysGlySerProTyrGlySer 440
Db 856 GGAATGGGATCTTTCATCTGTAGAAAGGAGAAAGAAAGAAATCCATATGTGTCA 915
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
Db 916 GCTGACGCTCAGAAACAGCGCTGTGGAGCAGATTAATATCCCTTTGCCAGGCATCAG 975
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
Db 976 TCGACGGAAATTTACCATCAGTATGACAAATGAAAAAGAGATGACACAAAAGTTGGATCTC 1035
QY 481 IleThrSerAspMetAla 486
Db 1036 ATCACTAGTATGATGGCA 1053
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RESULT 6

US-10-191-436A-7

; Sequence 7, Application US/10191436A

; Patent No. 6900031

GENERAL INFORMATION:

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; APPLICANT: Tasuku Honjo
; APPLICANT: Kei Tashiro
; APPLICANT: Kazuhiro Kobuke
; TITLE OF INVENTION: A NOVEL POLYPEPTIDE ESDN, POLYNUCLEOTIDES ENCODING THE POLYPEPTI
; FILE REFERENCE: 070993
; CURRENT APPLICATION NUMBER: US/10191,436A
; CURRENT FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2310
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; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(198)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (199)..(2310)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2310)
; US-10-191-436A-7
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Alignment Scores:

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Pred. No.: 1,24e-87 Length: 2310
Score: 867.50 Matches: 207
Percent Similarity: 54.63% Conservative: 94
Best Local Similarity: 37.57% Mismatches: 171
Query Match: 33.93% Indels: 79
DB: 3 Gaps: 17
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US-10-813-588-2 (1-487) x US-10-191-436A-7 (1-2310)

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QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
Db 241 CTTACATCCATCACTACCCATACCTATCTCTAACAGTACTGTGTGTAATGGGAGATT 300
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGlu---Ser 39
Db 301 CGAGTAAGACGGAGAAAGAATTCGCATCAAGTTCGGTGACTTTGCACATTGAAGATTCT 360
QY 40 GlnThrCysAlaSerAspTyrIleu---LeuPheThrSer-----SerSerAspGln 55
Db 361 GATTATTGTCCACTTAATACCTGAAATCTTTAATGGAATTGGAGTCAGACGAAACGGAA 420
QY 56 TyrGlyProTyrCysGly---SerMetThrValProLysGluLeuLeuAsnThrSer 74
Db 421 ATAGGCAAGTACTGTGGTCTGGGTTTACAATGAATCAGTCAATTGAGTCCAAAGGCAGT 480
QY 75 GluValThrValArgPheGluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThr 94
Db 481 GAAATCACAGTGTCTTCATGAGTGAATCCATGCTTCTGGTCGAGGATTTTGGGCTTCT 540
QY 95 TyrAlaSerSerAspHisProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeu 114
Db 541 TACTCAGTTATAGATAAACAAGATTTAATCAGTTGTTGGATCTGATCTATTAATTTTTG 600
QY 115 LysThrGluTyrSerLysPheCysProAlaGlyCysArgAspValAlaGlyAspIleSer 134
Db 601 GAACCTGAGTTCTAGTAAGTACTGCCCGAGCTGGCTGTCTGCTGCTTTTGTGTAATATCT 660
QY 135 GlyAsnMetValAspGlyTyrArgAspThrSerLeuLeuCysLysAlaIleHisAla 154
Db 661 GGAACGATTCCTCATGATATAGAGATTCTTCAACCGCTGTGTATGCTGGAATCCATGCA 720
QY 155 GlyIleIleAlaAspGluLeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSer 174
Db 721 GGAGTAGTGTAGATGTGGTGGCCAAATCAGCGTTGTGTATTAGCAAGACCCCA 780
QY 175 ArgTyrGluGlyIleLeuAlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLys 194
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Db 781 TATTACGAAGTTCTTTGGCCAAATGTCCTTCCATGGTGGTACTTATCTACGAGT 840
Qy 195 ArgPheLeuPheThrSerAsnGlyCysSerArgSerLeuSerPheGlu----- 210
Db 841 CTGTTTACATTTAAGACACTGGTGTCTATGGGACTTAGGGATGAGTCAGGTGATC 900
Qy 211 ProAspGlyGlnIleArgAlaSerSerTrpGlnSerValAsnGluSerGlyAspGln 230
Db 901 GCCGATCCCAAGATAACAGCATCATCTGTACTGGAGTGGACTGACCATGGGCGAGG 960
Qy 231 ValHisTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSerTrpAlaSerGly 250
Db 961 AACAGCTGAAACCCGAGAGGCGAGCTGAGAAAACCGGGGCTCCCTGGGTGCT--- 1017
Qy 251 AspSerSerAsnAsnHisLysProArgGluTrpLeuGluIleAspLeuGlyLys 270
Db 1018 TTTGCCACTGATGAGCAT-----CAGTGGCTGCAATGACCTTAATAGGAGAG 1068
Qy 271 LysIleThrGlyIleArgThrThrGlySerThrGlnSerAsnPheAsnPheTrpValLys 290
Db 1069 AAGATAACAGGCATGCTAACCACTGGATCTACCTGATAGAGCACAATTACTATGTGCT 1128
Qy 291 SerPheValMetAsnPheLysAsnAsnSerLysTrpLysThrTrpLysGlyIleVal 310
Db 1129 GCTACAGAGTTCTGTACAGTGCAGTGGCGCAGAAATGGACTGTGTACAGAGCCTGGT 1188
Qy 311 AsnAsnGluGluLysValPheGlnGlyAsnSerAsnPheArgAspProValGlnAsn 330
Db 1189 GCGGCTCAGCAGAGATATTTCAAGGAACAAGATTATCACAAAGGATGTTGCTAATAAC 1248
Qy 331 PheIleProPheValAlaArgTyrValArgValProGlnThrTrpHisGlnArg 350
Db 1249 TTTTGGCCACCAATTATTGACGTTTCAATTAGAGTGAACTGTCCAGTGGCAACAGAA 1308
Qy 351 IleAlaLeuLysValGluLeuIleGlyCysGlnIleThr----- 363
Db 1309 ATTGCCATAAGTGAATTTGCTGGGATGTCAGTTCACTCTGAAAGGTCGCTTCCAAAG 1368
Qy 364 -----GlnGlyAsnAspSerLeuValTrpArgLysThrSerGln 376
Db 1369 CTTACTCAACCTCCCCACCTCGGAACAGCAATAACCTC-----AAA 1410
Qy 377 SerThrSerValSerThrLys----- 383
Db 1411 AACACTACAGTTTCATCCCAACTAGTCTGGTCCCTTAATTTACTCAAGCACTCCAACCA 1470
Qy 384 -----LysGluAspGluThrIleThrArgProIleProSerGluThrSerThr 400
Db 1471 CGAAGTAGGAATGACCTTCTCTG-----CTGCCGCCCGCAGCAACTGCCACTCCT 1521
Qy 401 GlyIleAsnIleThrThr-----ValAlaIleProLeuVal 412
Db 1522 GATGTCAAAACACAGCACTGTGACTCCAGTGTGACCAAGATGTTGCACTGGCCGCGT 1581
Qy 413 LeuLeuValValLeuValPheAlaGlyMetGlyIlePheAlaAlaPhe----- 428
Db 1582 CTGGTTCGTGCTGTGCTATGCGCTCACCACACTCATCTATTCTAGTGTGCTTGG 1641
Qy 429 -----ArgLysLysLysLysLysGlySerProTyrGlySerAlaGluAlaGln 444
Db 1642 CATTTGGAGAAACAGAAAGAAAGCCGAAGGCACC---TATGATTTATCCCACTGGGAT 1698
Qy 445 LysThrAspCysTrpLysGlnIleLys-----TyrProPheAlaArgHisGlnSerAla 462
Db 1699 CGGGCAGCGCTGGTGGAAAGAGGTGAAGCAGCTTCTCCCTGCCCAATTCGGTGAACACGAG 1758
Qy 463 GluPheThrIleSerTyrAspAsnGlu-----LysGluMetThr 475
Db 1759 GAGACCGCAGTGGCTTACAGCAACAGTGAAGTTAGTCACTGAGCCCGGAGGAGTCAAG 1818
Qy 476 GlnLysLeuAspLeuIleThrSerAspMetAla 486
Db 486
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Db 1819 ACAGTGCTGCAAGCTGATTCTGCAGAAATACGCA 1851

RESULT 7

US-10-191-436A-9
; Sequence 9, Application US/10191436A
; Patent No. 6900031
; GENERAL INFORMATION:
; APPLICANT: Tasuku Honjo
; APPLICANT: Kei Tashiro
; APPLICANT: Kazuhiro Kobuke
; TITLE OF INVENTION: A NOVEL POLYPEPTIDE ESDN, POLYNUCLEOTIDES ENCODING THE POLYPEPT
; FILE OF INVENTION: UTILITY OF THE POLYPEPTIDE
; FILE REFERENCE: Q70993
; CURRENT APPLICATION NUMBER: US/10/191,436A
; CURRENT FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 2310
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-191-436A-9

Alignment Scores:
Pred. No.: 1,24e-87 Length: 2310
Score: 867.50 Matches: 207
Percent Similarity: 54.63% Conservative: 94
Best Local Similarity: 37.57% Mismatches: 171
Query Match: 33.93% Indels: 79
DB: 3 Gaps: 17

US-10-813-588-2 (1-487) x US-10-191-436A-9 (1-2310)

```
Qy 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
Db 241 CTTATCATCATCACTCACTCCACATACCTATCTTAACAGTACTGTGTGTAATGGGAGATT 300
Qy 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGlu---Ser 39
Db 301 CGAGTAAGACGGGAGAGAAGATTGCGATCACTAGTTCGGTGACTTTGACATTGAGATTCT 360
Qy 40 GlnThrCysAlaSerAspTyrLeu---LeuPheThrSer-----SerSerAspGln 55
Db 361 GATTATTGTCACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
Qy 56 TyrGlyProTyrCysGly---SerMetThrValProLysGluLeuLeuLeuAsnThrSer 74
Db 421 ATAGGCAAGTACTGTGGTCTGGGTTTACAAATGAATCAGTCAATTGAGTCCAAAGCAGT 480
Qy 75 GluValThrValArgPheGluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThr 94
Db 481 GAAATCACAGTCTGTTTCATGATGGAATCCATGCTTCTGGTCGAGGATTTTGGCTTCT 540
Qy 95 TyrAlaSerSerAspHisProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeu 114
Db 541 TACTCAGTTATAGATAAAACAAAGATTTAATCACTGTTTGGATCTGTATCTAATTTTGG 600
Qy 115 LysThrGluTyrSerLysPheCysProAlaGlyCysArgAspValAlaGlyAspIleSer 134
Db 601 GAACCTGAGTTTCAGTAAGTACTGCCACGCTGCTCTGCTCCCTTTTCTCTGAAATATCT 660
Qy 135 GlyAsnMetValAspGlyTyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAla 154
Db 661 GGAACGATTCCTCATGGATATAGATTCTTCCCGCTGTGTATGGTGGATTCATATCA 720
Qy 155 GlyIleIleAlaAspGluLeuGlyGlyGlnIleSerValLeuGlnArgLysGlyLeuSer 174
Db 721 GGAGTAGTGTCAAGTGTCTGGGTGCCAAATCAGCGTTGTGATTAGCAAAAGCCACCCCA 780
Qy 175 ArgTyrGluGlyIleLeuAlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLys 194
Db 781 TATTACGAAGATTTCTTTGGCCAAATGTCACTTCCATGGTGGGATACTTATCTACGAGT 840
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QY 195 ArgPheLeuPheThrSerSerLeuGlyCysSerArgSerLeuSerPheGlu----- 210
Db 841 CTGTTTACATTTAAGACAAGTGGTTGCTATGGACTCTAGGATGGAGTCAGGTGTGATC 900
QY 211 ProAspGlyGlnIleArgAlaSerSerSerTrpGlnSerValAsnGluSerGlyAspGln 230
Db 901 GCGGATCCCCAGATAACAGCATCTCTGACTGGAGTGAGTACACACATGGGCGAGGAG 960
QY 231 ValHisTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSerTrpAlaSerGly 250
Db 961 AACAGCTGGAACCCGAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1017
QY 251 AspSerSerAsnAsnHisLysProArgGluTrpLeuGluIleAspLeuGlyGluLysLys 270
Db 1018 TTTGCCACTGATGAGCAT-----CAGTGGCTGCAAAATTGACCTTAATAAGGAGAAG 1068
QY 271 LysIleThrGlyIleArgThrGlySerThrGlnSerAsnPheAsnPheThrValLys 290
Db 1069 AAGTAACAGGCACTGTAACCTGATCTACCTGATGAGGACACATTAATGATGTCT 1128
QY 291 SerPheValMetAsnPheLysAsnAsnAsnSerLysTrpLysThrTrpLysGlyIleVal 310
Db 1129 GCCTACAGAGTCTGTACAGTGCAGATGGCGAGAAATGGACTGTGTACAGAGGCGCTGT 1188
QY 311 AsnAsnGluLysValPheGlnGlyAsnSerAsnPheArgAspProValGlnAsnAsn 330
Db 1189 GCGGCTCAGGACAAGATATTTCAAGGAAACAAAGATTATCACAAGGATGTTCGTATAAC 1248
QY 331 PheIleProPheValAlaArgTyrValArgValValProGlnThrTrpHisGlnArg 350
Db 1249 TTTTTCGCCCAATTATGACGCTTTCATTAGAGTGAACCTGTCCAGTGGCAACAGAAA 1308
QY 351 IleAlaLeuLysValGluLeuIleGlyCysGlnIleThr----- 363
Db 1309 ATTGCCATGAAGTGAATTGCTGGGATGTGCTGCTGCAAGTCCGCTTCCAAAG 1368
QY 364 -----GlnGlyAsnAspSerLeuValTrpArgLysThrSerGln 376
Db 1369 CTTACTCAACCTCCCGCACCTCGGACAGCAATACCTC-----AAA 1410
QY 377 SerThrSerValSerThrLys----- 383
Db 1411 AACCTACAGTTTCATCCCAAACTAGTGTGCGCCCTAAATTTACTCAAGCACTCCCAACCA 1470
QY 384 -----LysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr--- 400
Db 1471 CGAAGTAGGAATGACCTTCCTCTG-----CTGCGGCGCCGACAGCAACTGCCACTCCT 1521
QY 401 GlyIleAsnIleThr-----ValAlaIleProLeuVal 412
Db 1522 GATGTCAAAAACACGACTGTGACTCCAGTGTGACCAAAAGATGTGCACTGCGCGCGGTT 1581
QY 413 LeuLeuValValLeuValPheAlaGlyMetGlyIlePheAlaAlaPhe----- 428
Db 1582 CTGCTCTGCTGTGTCATGGCCCTCACCACACTCATCTCTATCTAGTGTGTGCTGG 1641
QY 429 -----ArgLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 444
Db 1642 CATTGGAGAAACAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1698
QY 445 LysThrAspCysTrpLysGlnIleLys-----TyrProPheAlaArgHisGlnSerAla 462
Db 1699 CGGGCAGGCTGGTGGAAAGAGTGAAGCAGCTTCTCCCTCCCAATCGGTGGAAACAGGAG 1758
QY 463 GluPheThrIleSerTrpAspAsnGlu-----LysGluMetThr 475
Db 1759 GAGACGCGATGGCTACAGCAACAGTGAAGTTAGTACCTGACCGCGGAGGAGTCAAG 1818
QY 476 GlnLysLeuAspLeuIleThrSerAspMetAla 486
Db 1819 ACAGTGCTGCAAGCTGATTCTGCAGAAATACGCA 1851
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RESULT 8

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US-10-191-436A-1
; Sequence 1, Application US/10191436A
; Patent No. 6900031
; GENERAL INFORMATION:
; APPLICANT: Tasuku Honjo
; APPLICANT: Kei Tashiro
; APPLICANT: Kazuhiko Kobuke
; TITLE OF INVENTION: A NOVEL POLYPEPTIDE ESDN, POLYNUCLEOTIDES ENCODING THE POLYPEPTIDE
; FILE REFERENCE: Q70993
; CURRENT APPLICATION NUMBER: US/10/191,436A
; CURRENT FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2328
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(198)
; NAME/KEY: mat_peptide
; LOCATION: (199)..(2328)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2328)
US-10-191-436A-1
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Alignment Scores:
Pred. No.: 7,79e-87 Length: 2328
Score: 860.50 Matches: 206
Percent Similarity: 54.33% Conservative: 95
Best Local Similarity: 37.18% Mismatches: 170
Query Match: 33.65% Indels: 83
DB: Gaps: 17
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US-10-813-588-2 (1-487) x US-10-191-436A-1 (1-2328)

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QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
Db 250 CTTACATCCATAAACTACCCACAGACCTATCCCAACAGACACTGTTGTGAATGGGAGATC 309
QY 21 ThrValProGlyGlyLysArgLeuLeuArgLeuGlyAspLeuAspIleGlu---Ser 39
Db 310 CGTGTAAAGATGGGAGAGAGATTCGCATCAAAATTTGGTGACTTTGACATTTGAAGATTCT 369
QY 40 GlnThrCysAlaSerAspTyrLeuLeuPheThrSer-----SerSerAspGln 55
Db 370 GATTCCTGTGACTTTAATTTACTTTGAGAAATTTAATGGAATGGAGTCAGCAGAACTGAA 429
QY 56 TyrGlyProTyrCysGly---SerMetThrValProLysGluLeuLeuAsnThrSer 74
Db 430 ATAGGCAATACTGTGCTGGGTTGCAAAATGAACCAATTCATTTGAATCAAAAGGCAAT 489
QY 75 GluValThrValArgPheGluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThr 94
Db 490 GAAATCACATTCGTGTTTCATGAGTGAATTCATGTTCTGGACGCGGATTTTGGCCTCA 549
QY 95 TyrAlaSerSerAspHisProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeu 114
Db 550 TACTCTGTTATAGATAAACAAGATCTAATTAATCTTTGTTGGACACTGCATCCCAATTTTGG 609
QY 115 LysThrGluLysSerLysPheCysProAlaGlyCysArgAspValAlaGlyAspIleSer 134
Db 610 GAACCTGAGTTCAGTAAGTACTGCCAGCTGGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCT 669
QY 135 GlyAsnMetValAspGlyTyrArgAspThrSerLeuLeuCysLysAlaIleHisAla 154
Db 670 GGAACAATTCCTCATGGATATAGAGATTCCTGCCATTGTGTCATGCTGGTGTGCAATGCA 729
QY 155 GlyIleIleAlaAspGluLeuGlyGlnIleSerValLeuGlnArgLysGlyIleSer 174
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Db 730 GGAGTAGTGTCAACACAGTTGGCGGCCAAATCAGTGTGTAAATAGTAAAGGTATTCCC 789
QY 175 ArgTyrGluGlyIleLeuAlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLys 194
Db 790 TATTATGAAGTCTTGTGGTCAACAGTCACTCTGTGTGGGACACTTATCTACAGT 849
QY 195 ArgPheLeuPheThrSerAsnGlyCysSerArgSerLeuSerPheGlu----- 210
Db 850 CTTTTTACATTTAAGACAGTGGATGTATGAACACTGGGATGGATCTGTGTGATC 909
QY 211 ProAspGlyGlnIleArgAlaSerSerTrpGlnSerValAsnGluSerGlyAspGln 230
Db 910 CGCGATCCTCAATAACAGCATCATCTGCTGGAGTGGACTCACCACACAGGCGAAG 969
QY 231 ValHisTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSerTrpAlaSerGly 250
Db 970 AACAGTTGGAAACCCAAAAAGCGAGCTGAAAAACCTGGACCGCTGGGCTGCTTT 1029
QY 251 AspSerSerAsnAsnHisLysProArgGluTrpLeuGluIleAspLeuGlyGluLys 270
Db 1030 GCCACTGTATGAA-----TACCAGTGTGTACAAATAGATTGTAATAGGAAG 1077
QY 271 LysIleThrGlyIleArgThrThrGlySerThrGlnSerAsnPheAsnPheTyrValLys 290
Db 1078 AAAATACAGGCAATTAACCACTGGATCCACCATGCTGGAGCACAATTTACTATGTCT 1137
QY 291 SerPheValMetAsnPheLysAsnAsnSerLysTrpLysThrTyrLysGlyIleVal 310
Db 1138 GCCTACAGATCTCTGACAGTGTATGATGGCAGAAATGACTGTGTACAGAGCCTGGT 1197
QY 311 AsnAsnGluGluLysValPheGlnGlyAsnSerAsnPheArgAspProValGlnAsnAsn 330
Db 1198 GTGGAGCAAGATAAGATATTTCAGGAAACAAAGATTATCACCAGGATGTGCGTAATAAC 1257
QY 331 PheIleProPheValAlaAlaArgTyrValArgValValProGlnThrTrpHisGlnArg 350
Db 1258 TTTTTCGCCCAATATTATGCATGCTTTATTAGAGTGAATCTTACCCTACCAATGGCAGAGAA 1317
QY 351 IleAlaLeuLysValGluLeuIleGlyCysGln----- 361
Db 1318 ATGTCCATGAATGAGTGTCTCGATGTCACTTTATTCCTTAAGGTGTCTCTCAAAA 1377
QY 362 IleThrGln-----GlyAsnAspSerLeuValTrpArgLysThrSer 375
Db 1378 CTTACTCAACCTCCACTCTCTCGAACACAGCAATGAC-----CTCAAAACACT 1425
QY 376 GlnSerThrSerValSerThrLysGluAspGluThrIleThrArgProIle----- 393
Db 1426 ACAGCCCTCCCAAAATAGCAAAAGTCTGCGCCCAAAATTTACGCAACCACTTACAACCT 1485
QY 394 -----ProSerGluGluThr-----SerThrGlyIleAsn 403
Db 1486 CGCAGTAGCAATGAATTTCTGCACAGACAGACAAACAACTGCCAGTCTGTATATCAGA 1545
QY 404 IleThrThr-----ValAlaIleProLeuValLeuVal 415
Db 1546 AATACTACGTAACTCCAAATGTAAACAAAGATGTAGCGTGTGCTGCACTTCTGTCCCT 1605
QY 416 ValLeuValPheAlaGlyMetGlyIlePheAlaAlaPhe----- 428
Db 1606 GTGCTGGTCAATGCTCTCACTCTCATTTCTCATATTAGTGTGTGCTGGCAGCTGGAGA 1665
QY 429 ---ArgLysLysLysLysLysGlySer-----ProTyrGlySerAlaGluAlaGln 444
Db 1666 AACAGAAAGAAAAAACTAGAGCACCCTATGACTTACCTTACTGG-----GAC 1713
QY 445 LysThrAspCysTrpLysGlnIleLysTyr----- 454
Db 1714 CGGGCAGGTTGGTGGAAAGAAATGAAGCAGTTCCTTCCTGCAAAAGCAGTGACCATGAG 1773
QY 455 -----ProPheAlaArgHisGlnSerAlaGluPheThrIleSerTyrAspAsnGluLys 472
Db 1774 GAAACCCCA---GTTTCGCTATAGCAGCAGCGAA-----GTTAATCACCCTGAGTCCAAGA 1824

QY 473 GluMetThrGlnLysLeuAspLeuIleThrSerAspMetAla 486
Db 1825 GAAGTCACCACAGTGTGCGAGTGTGCTGCGAGAGTATGCT 1866

RESULT 9

US-10-191-436A-3
; Sequence 3, Application US/10191436A
; Patent No. 6900031
; GENERAL INFORMATION:
; APPLICANT: Tasuku Honjo
; APPLICANT: Kei Tashiro
; APPLICANT: Kazuhiro Kobuke
; TITLE OF INVENTION: A NOVEL POLYPEPTIDE ESDM, POLYNUCLEOTIDES ENCODING THE POLYPEPTIDE
; FILE REFERENCE: Q70993
; CURRENT APPLICATION NUMBER: US/10/191,436A
; CURRENT FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2328
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-436A-3

Alignment Scores:
Pred. No.: 7,79e-87 Length: 2328
Score: 860.50 Matches: 206
Percent Similarity: 54.33% Conservative: 95
Best Local Similarity: 37.18% Mismatches: 170
Query Match: 33.65% Indels: 83
DB: 3 Gaps: 17

US-10-813-588-2 (1-487) x US-10-191-436A-3 (1-2328)

QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
Db 250 CTTACATCCATAAACTACCCACAGACCTATCCACAGCAGCTGTTGTGAATGGGAGATC 309
QY 21 ThrValProLysGlyLysArgLeuLeuArgLeuGlyAspLeuAspIleGlu-----Ser 39
Db 310 CGTGTAAAGATGGGAGAGAGAGTTCGCATCAAAATTTGTGTGACTTTGACATTTGAAGATTCT 369
QY 40 GlnThrCysAlaSerAspTyrLeuLeuPheThrSer-----SerSerAspGln 55
Db 370 GATTCCTGTGCACTTAAATTACTTGAGAAATTAATGAATGGAGTTCAGCAGAACTGAA 429
QY 56 TyrGlyProTyrCysGly---SerMetThrValProLysGluLeuLeuLeuAsnThrSer 74
Db 430 ATAGGCAATACTGTGGTCTGGGTTGCAAAATGAACCATTCATTTGAATCAAAAGGCAAT 489
QY 75 GluValThrValArgPheGluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThr 94
Db 490 GAAATCACATTCCTGTTCTATGATGGAATCCATGTTCTGGACGGGATTTTGGCCTCA 549
QY 95 TyrAlaSerSerAspHisProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeu 114
Db 550 TACTCTGTATAGATAAAACAAGATCTAATTACTTGTGTTGGCAGCTGCATCCCAATTTTGG 609
QY 115 LysThrGluTyrSerLysPheCysProAlaGlyCysArgAspValAlaGlyAspIleSer 134
Db 610 GAACTGTAGTTACAGTAAGTACTGCCAGCTGTTGTCTGCTCTCTTCTCTGAGATATCT 669
QY 135 GlyAsnMetValAspGlyTyrArgAspThrSerLeuLeuCysGlyAlaIleHisAla 154
Db 670 GGAACAATTCCTCATGATATAGAGATTCCTCGCCATTTGTGATGCTGCTGTCATGCA 729
QY 155 GlyIleIleAlaAspGluLeuGlyGlnIleSerValLeuGlnArgLysGlyIleSer 174
Db 730 GGAGTAGTGTGTAACACCGTTGGCGGCAAAATCAGTGTGTTGTAATTAGTAAGATTTCCC 789
QY 175 ArgTyrGluGlyIleLeuAlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLys 194

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Db      790 TATTATGAAGTCTTTGGCTAAACACGTCACATCTGTGGTGGGACACTTATCTACAAGT 849
Qy      195 ArgPheLeuPheThrSerAsnGlyCysSerArgSerLeuSerPheGlu----- 210
Db      850 CTTTTCATATTAAGACAAGTGGATGTTATGGAAACACTGGGATGGAGTCTGGTGTGATC 909
Qy      211 ProAspGlyGlnIleArgAlaSerSerTrpGlnSerValAsnGlnSerGlyAspGln 230
Db      910 CGCGATCCTCAATAACAGCATCTGTCTGTGGAGTCACTACCCACAGCGCAAGAG 969
Qy      231 ValHisTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSerTrpAlaSerGly 250
Db      970 AACAGTTGGAAACCCAAAGCCAGCGTGAAACACCTGACCGCTTGGGGTGTCTTT 1029
Qy      251 AspSerSerAsnAsnHisLysProArgGluTrpLeuGluIleAspLeuGlyGluLys 270
Db      1030 GCCACTGATCA-----TACCAGTGGTTACAATAGATTTGAATAAGGAAG 1077
Qy      271 LysIleThrGlyIleArgThrThrGlySerThrGlnSerAsnPheAsnPheThrValLys 290
Db      1078 AAAATAACAGCATTAACCACTGGATCCACCATCGTGAGCACAATTAATACTATGTGTCT 1137
Qy      291 SerPheValMetAsnPheLysAsnAsnSerLysTrpLysThrLysGlyIleVal 310
Db      1138 GCCTCAGAAATCTGTACAGTGTATGATGGCAGAAATGGACTGTGTACAGAGCCTGGT 1197
Qy      311 AsnAsnGluLysValPheGlnGlyAsnSerAsnPheArgAspProValGlnAsnAsn 330
Db      1198 GTGGAGCAGATGAATATTTCAAGGAACAAGATTAATCACCAGGATGTGGTATATAC 1257
Qy      331 PheIleProPheValAlaArgTyrValArgValProGlnThrTrpHisGlnArg 350
Db      1258 TTTTTCGCCAATATTATGCACGTTTATTAGAGTGAATCCTACCCAAATGGCAGCAGAAA 1317
Qy      351 IleAlaLeuLysValGluLeuIleGlyCysGln----- 361
Db      1318 ATTGGCAATGAATGGAGCTGCTCGGATGTCATTTATTCCTAAAGTGCTCTCCAAA 1377
Qy      362 IleThrGln-----GlyAsnAspSerLeuValTrpArgLysThrSer 375
Db      1378 CTTACTCACTCCACTCTCTCGGAACAGCAATGAC-----CTCAAAACACT 1425
Qy      376 GlnSerThrSerValSerThrLysLysGluAspGluThrIleThrArgProIle----- 393
Db      1426 ACAGCCCTCCAAAATAGCAAAAGGTCTGCGCCCAAAATTTACGCAACCACTACAACCT 1485
Qy      394 -----ProSerGluGluThr-----SerThrGlyIleAsn 403
Db      1486 CGCAGTAGCAATGAATTTCTCGACAGACAGACAACAACACTGCCAGTCTCTGATATCAGA 1545
Qy      404 IleThrThr-----ValAlaIleProLeuValLeuVal 415
Db      1546 AATACTACCGTAATCCAAATGTAACCAAGAGATGTAGCGTGGCTGCAGTCTTGTCCCT 1605
Qy      416 ValLeuValPheAlaGlyMetGlyIlePheAlaAlaPhe----- 428
Db      1606 GTGCTGTCTACTGTGCTCACTACTCTCATCTCTCATATTAGTGTGTGTGGCACTGGAGA 1665
Qy      429 ---ArgLysValValLysLysGlySer-----ProTyrGlySerAlaGluAlaGln 444
Db      1666 AACAGAAAGAAAAAATCTGAAGGACCACTATGACTTACTTACTGG-----GAC 1713
Qy      445 LysThrAspCysTrpLysGlnIleLysTyr----- 454
Db      1714 CGGGCAGTTGGTGGAAAGGATGAACAGCTTTCTCTCTCAAAAGCAGTGGACCATGAG 1773
Qy      455 -----ProPheAlaArgHisGlnSerAlaGluPheThrIleSerTyrAspAsnGluLys 472
Db      1774 GAAACCCCA---GTTTCGCTATAGCAGCAGCGAA-----GTTAATCACTACCTGAGTCCAAGA 1824
Qy      473 GluMetThrGlnLysLeuAspLeuIleThrSerAspMetAla 486
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Db      1825 GAAGTCACCACAGTCTGCTGAGGCTGACTCTGCAGAGATATGCT 1866
RESULT 10
US-10-191-436A-4
; Sequence 4, Application US/10191436A
; Patent No. 6900031
; GENERAL INFORMATION:
; APPLICANT: Tasuku Honjo
; APPLICANT: Kei Tashiro
; APPLICANT: Kazuhiro Kobuke
; TITLE OF INVENTION: A NOVEL POLYPEPTIDE ESDN, POLYNUCLEOTIDES ENCODING THE POLYPEPTIDE
; TITLE OF INVENTION: UTILITY OF THE POLYPEPTIDE
; FILE REFERENCE: Q70993
; CURRENT APPLICATION NUMBER: US/10/191,436A
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2310
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(198)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (199)..(2310)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2310)
US-10-191-436A-4
Alignment Scores:
Pred. No.: 2,18e-86 Length: 2310
Score: 856.50 Matches: 203
Percent Similarity: 54.66% Conservative: 96
Best Local Similarity: 37.11% Mismatches: 177
Query Match: 33.50% Indels: 71
DB: 14

US-10-813-588-2 (1-487) x US-10-191-436A-4 (1-2310)
Qy      1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
Db      241 CTTACATCCATCAACTACCCATACCTATCTCTAACAGCACTGTGTGTAATGGGAGATT 300
Qy      21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGlu---Ser 39
Db      301 CGAGTCAGGACGGAGAAAGGATTCGCATCAAAATTCGGTGACTTTGCACATTGAAGATTCT 360
Qy      40 GlnThrCysAlaSerAspTyrLeu---LeuPheThrSer-----SerSerAspGln 55
Db      361 GATTATTGTGCACCTTAATACCTGAAAATCTTTAATGGAAATTTGGAGTCAGCAGAACGGAA 420
Qy      56 TyrGlyProTyrCysGly---SerMetThrValProLysGluLeuLeuLeuAsnThrSer 74
Db      421 ATAGCAAAATACTGTGTGTGGTGTTCACAAATGAATCAGTCAATTCAGTCCAAAGCAGT 480
Qy      75 GluValThrValArgPheGluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThr 94
Db      481 GAAGTCACAGTGTCTGTTTCATGATGGACCCATCGCTGCTGGCGAGAGATTTTGGCTTCA 540
Qy      95 TyrAlaSerSerAspHisProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeu 114
Db      541 TACTCAGTTATAGATAAAGAAGATTTAATCACTTGTTTGGATACCTGATCTATCTAATTTTGG 600
Qy      115 LysThrGluTyrSerLysPheCysProAlaGlyCysArgAspValAlaGlyAspIleSer 134
Db      601 GAACCAAGTTTCATGTAAGTACTGCCAGCTGGCTGTCTTTTGGCTTTTGGCTGTAATATCT 660
Qy      135 GlyAsnMetValAspGlyTyrArgAspThrSerLeuLeuCysLysAlaIleHisAla 154
Db      661 GGAAACAATTCTCATGGATACAGAGATTTCTTACCATTGTGTATGGTGGATCCATGCA 720
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QY 155 GlyIleAlaAspGluLeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSer 174
DB 721 GGAGTAGTCAAAAGTCTGGTGGCCAAATCAGCATTTGATTAGCAAGAGACCCCA 780
QY 175 ArgTyrGluGlyIleLeuAlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLys 194
DB 781 TATTATGAAGCTCTTTGGCCAAATGTCACCTCCACGGTGGGATCTTATCTGCAAGT 840
QY 195 ArgPheLeuPheThrSerAsnGlyCysSerArgSerLeuSerPheGlu----- 210
DB 841 CTGTTTACATTTAAGCAAGTGTGCTATGGAGCTCTGGGATGGAGTCTGGTGTGATT 900
QY 211 ProAspGlyGlnIleArgAlaSerSerTyrGlnSerValAsnGluSerGlyAspGln 230
DB 901 GCCGATCCCAAGATACAGATCTGTCTGACGTGGAGTGGACTGACACATGGGCGAGGAG 960
QY 231 ValHisTyrSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSerTyrAlaSerGly 250
DB 961 AACAGCTGCACAGCGGAGGAGCGAGCTGAGAAACCCGGGCTCCCTGGGCTGCT--- 1017
QY 251 AspSerSerAsnAsnHisLysProArgGluTyrLeuGluIleAspLeuGlyLysLys 270
DB 1018 TTTGCCACTGATGAGCAT-----CAGTGGCTGCAGATAGACCTTAACAAGGAGAG 1068
QY 271 LysIleThrGlyIleArgThrThrGlySerThrGlnSerAsnPheAsnPheTyrValLys 290
DB 1069 AAGATTAACAGGTATCTGATACCACTGGTCTTACCATGATAGACACAGTTACTATGTGCT 1128
QY 291 SerPheValMetAsnPheLysAsnAsnSerLysTyrLysThrTyrLysGlyIleVal 310
DB 1129 GCCTACAGAGTCTGTACAGTACGATGGCAGAGATGGACTGTGTACAGAGAACCTGGT 1188
QY 311 AsnAsnGluGlyLysValPheGlnGlyAsnSerAsnPheArgAspProValGlnAsnAsn 330
DB 1189 GTGGACGAGGACAGATATTTCAAGGAAACAAAGATTATCACAAAGGATGTTGCTATAAC 1248
QY 331 PheIleProPheValAlaArgTyrValArgValValProGlnThrTyrHisGlnArg 350
DB 1249 TTTTGGCCACCAATATTGACGTTTCATTAGTAGTGAACCTGTCAGTGGCAGACAGAA 1308
QY 351 IleAlaLeuLysValGluLeuIleGlyCysGlnIleThr----- 363
DB 1309 ATTGCCATGAAGTGAACCTGCTCGATGTGCTGATTTACTCTCAAGGTGCGCTTCCAAAG 1368
QY 364 -----GlnGlyAsnAspSerLeuValTyrArgLysThrSer----- 375
DB 1369 CTTACTCCACCTCTCTCGGAACGCAATAAC-----CTCAGAAATACTACAGCTCGT 1419
QY 376 -----GlnSerThr 378
DB 1420 CCCAACTAGGTAAAGGTGTGGCCCTAAATTTACTCAAGTGTCCAACTCGAAGTAGG 1479
QY 379 SerValSerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThr 398
DB 1480 AATGAACCTCTCTGTCAGCGCGGAGAGCAACTACCCTCTGATATATAAAACACAGACT 1539
QY 399 SerThrGlyIleAsnIleThrThrValAlaIleProLeuValLeuValValLeuVal 418
DB 1540 GTAACCTCCAGTGTAAACCAAGATGTCGCACTGGCTGCGCTTCTGCTGCTGCTGCTG 1599
QY 419 PheAlaGlyMetGlyIlePheAlaAlaPhe-----ArgLys 430
DB 1600 ATGGCCCTCACCACTATCTCTCATCTTAGTGTGTGCTGGCAGTGGAGAACAGAGAG 1659
QY 431 LysLysLysLysGlySerProTyrGlySerAlaGluAlaGlnLysThrAspCysTyrLys 450
DB 1660 AAGAAACTGAAGCGCC---TATGATTATCCCACTGGGATCGGCAGGTGGTGGAAA 1716
QY 451 GlnIleLysTyrProPhe-----AlaArgHis 459
DB 1717 GGAATGAAGCAGCTTCTCCCTGCCAAGTGGTGGACCGAGGAGACGCGCAGTGGCGCTAC 1776

QY 460 GlnSerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAsp 479
DB 1777 ACAGTAGTGAA-----GTCACTCACCTGAGTGGCAGGGAAGTACCACAGTGTGTCAG 1830
QY 480 LeuIleThrSerAspMetAla 486
DB 1831 GCCGACTCTGCAGAATATGCA 1851
RESULT 11
US-10-191-436A-6
; Sequence 6, Application US/10191436A
; Patent No. 6900031
; GENERAL INFORMATION:
; APPLICANT: Tasuku Honjo
; APPLICANT: Kei Tashiro
; APPLICANT: Kazuhiro Kobuke
; TITLE OF INVENTION: A NOVEL POLYPEPTIDE ESDN, POLYNUCLEOTIDES ENCODING THE POLYPEPT
; FILE REFERENCE: Q70993
; CURRENT APPLICATION NUMBER: US/10/191,436A
; CURRENT FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 2310
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-191-436A-6
Alignment Scores:
Pred. No.: 2,18e-86 Length: 2310
Score: 856.50 Matches: 203
Percent Similarity: 54.66% Conservative: 96
Best Local Similarity: 37.11% Mismatches: 177
Query Match: 33.50% Indels: 71
DB: 3 Gaps: 14
US-10-813-588-2 (1-487) x US-10-191-436A-6 (1-2310)
QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB 241 CTTATCATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 300
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyValAspLeuAspIleGlu---Ser 39
DB 301 CGAGTCAGACCGGAGAGAGGATTCGATCAAAATTCGGTGCATTTGACATTTGAAGATTCT 360
QY 40 GlnThrCysAlaSerAspTyrLeu---LeuPheThrSer-----SerSerAspGln 55
DB 361 GATTATTGTACCTTAATTTACCTGAAATCTTTAATGGAATTTGGAGTCAGCAGAACGGAA 420
QY 56 TyrGlyProTyrCysGly---SerMetThrValProLysGluLeuLeuLeuAsnThrSer 74
DB 421 ATAGGCAAAATACTGTGGTCTGGGTTTACAAATGAATCAGTCAATGAGTCCAAAGCAGT 480
QY 75 GluValThrValArgPheGluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThr 94
DB 481 GAAGTCACAGTCTGTTTATGAGTGGACCCATGCTGCTGGCGAGGATTTTGGCTTCA 540
QY 95 TyrAlaSerSerAspHisProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeu 114
DB 541 TACTCAGTTATAGATAAAGAAGATTAAATCACTGTTTGGATACTGTATCTAATTTTGG 600
QY 115 LysThrGluTyrSerLysPheCysProAlaGlyCysArgAspValAlaGlyAspIleSer 134
DB 601 GAACCAAGAGTTCAGTAAGTACTGCCAGCTGCTGCTTTTGGCTTTTCTGCTGAAATATCT 660
QY 135 GlyAsnMetValAspGlyTyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAla 154
DB 661 GGAACAAATTCCTCATGATACAGATTTCTTCCATTTGTATGCTGCTGGAATCCATGCA 720
QY 155 GlyIleIleAlaAspGluLeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSer 174

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Db 721 GGAGTAGTGTAACACTGGTGGTGGCCAAATCAGCATTTGTGATTAGCAAGAGGCCCA 780
QY 175 ArgTyrGluGlyLeuAlaAenGlyValLeuSerArgAspGlySerLeuSerAspLys 194
Db 781 TATTATGAAGCTCTTTGGCCAAACATGTCTCCACGGTGGGATACTTATCTGCAAGT 840
QY 195 ArgPheLeuPheThrSerAenGlyCysSerArgSerLeuSerPheGlu----- 210
Db 841 CTGTTTACATTTAAGACAAGTGGTGTCTATGGGACTCTGGGGATGGAGTCTGTGTGATT 900
QY 211 ProAspGlyGlnIleArgAlaSerSerTrpGlnSerValAenGluSerGlyAepGln 230
Db 901 GCGGATCCCGAGATAACAGATCGTCTGCATCGAGTGGAGTACACACATGGGGCAGGAG 960
QY 231 ValHisTrpSerProGlyGlnAlaArgLeuGlnAenGlnGlyProSerTrpAlaSerGly 250
Db 961 AACAGCTGGACAGCGAGGAGCCGAGCTGAGAAACCCGGGCTCCCTGGGCTGCT--- 1017
QY 251 AspSerSerAenAenHisLysProArgGluTrpLeuGluIleAspLeuGlyLysLys 270
Db 1018 TTTGCCACTGATGAGCAT-----CAGTGGCTGCAGATAGACCTTAACAGGAGAAG 1068
QY 271 LyeIleThrGlyIleArgThrThrGlySerThrGlnSerAenPheAenPheTyrValLys 290
Db 1069 AAGTAAACAGGTATCTTAACCTAGCTGGGTCTACCATGATGAGAACACAGTACTATGTGCT 1128
QY 291 SerPheValMetAenPheLysAenAenAenSerLysTrpLysThrTyrLysGlyIleVal 310
Db 1129 GCCTACAGAGTCTGTACAGTACGAGTGGCGAGAGATGAGTGTGTACAGAGAACCTGTT 1188
QY 311 AenAenGluLysValPheGlnGlyAenSerAenPheArgAspProValGlnAenAen 330
Db 1189 GTGGACGAGCAAGATATTTCAAGGAAACAAAGATTATCACAAGGATGTTCTGTAATAAC 1248
QY 331 PheIleProProlleValAlaAaTyrValArgValValProGlnThrTrpHisGlnArg 350
Db 1249 TTTTGGCCCAATTTATGACGCTTTTCATTAGAGTGAACCTCTCCAGTGGGCAAGAAA 1308
QY 351 IleAlaLeuLysValGluLeuIleGlyCysGlnIleThr----- 363
Db 1309 ATTGCCATGAAGTGAAGTCTCGGATGTCAGTTTACTCTCAAGTGCCTTCACAAAG 1368
QY 364 -----GlnGlyAenAspSerLeuValTrpArgLysThrSer----- 375
Db 1369 CTTACTCCACTCTCTCGAACCGCAATAAC-----CTCAGAAATACTACAGCTCGT 1419
QY 376 -----GlnSerThr 378
Db 1420 CCCAACTAGTAAAGTGTGGCCCTAAATTTACTCAAGTGTCTCCACCTCGAAGTAGG 1479
QY 379 SerValSerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThr 398
Db 1480 AATGAATCTCTGTGCAGCGCGGAGACAACTACCACTCTGATATATAAAACACGACT 1539
QY 399 SerThrGlyIleAenIleThrThrValAlaIleProLeuValLeuValValLeuVal 418
Db 1540 GTAACCTCCAGTGTAAACAAAGATGTGCGACTGCTGCCGTCTGTGCTGCTGCTGCTG 1599
QY 419 PheAlaGlyMetGlyIlePheAlaAlaPhe-----ArgLys 430
Db 1600 ATGGCCCTCACCACACTCATCTCTAGTGTGTGCTGGCACTGGAGAACACAGGAAG 1659
QY 431 LysLysLysLysGlySerProTyrGlySerAlaGluAlaGlnLysThrAspCysTrpLys 450
Db 1660 AAGAAACTCAAGCGGCC---TATGATTATCCCACTGGGATCGGCGAGTGTGTGGAAA 1716
QY 451 GlnIleLysTyrProPhe-----AlaArgHis 459
Db 1717 GGAATGAAGCGCTTCTCCCTGCCAAGTGGTGGACCAAGAGAGAGCGCAGTGGCGCTAC 1776
QY 460 GlnSerAlaGluPheThrIleSerTyrAenAenGluLysGluMetThrGlnLysLeuAasp 479
Db 1777 AGCACTAGTGAA-----GTCACTGCTGAGTGCAGGGAAGTCAACACAGTGTGCTGAG 1830
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QY 480 LeuIleThrSerAspMetAla 486
Db 1831 GCGGACTCTGCAGAAATATGCA 1851

RESULT 12
US-09-116-473-1
; Sequence 1, Application US/09116473
; Patent No. 6428965
; GENERAL INFORMATION:
; APPLICANT: Kolodkin, Alex
; APPLICANT: Ginty, David
; TITLE OF INVENTION: SEMAPHORIN RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Banner & Witcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/116,473
; FILING DATE: 17-JUL-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/052,762
; FILING DATE: 17-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 01107.74973
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3371 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-116-473-1

Alignment Scores:
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Score: 331.50 Matches: 112
Percent Similarity: 40.13% Conservative: 73
Best Local Similarity: 24.30% Mismatches: 174
Query Match: 12.96% Indels: 102
DB: 3 Gaps: 17

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Db 429 ATCACTTCCCGAGGTATCCCGCCAGGACTATCCCTCTCACAGNACTGTAGTGGTGTGC 488
QY 21 ThrValProLys---GlyLysArgLeuIleLeuArgLeuGly---AspLeuAspIleGlu 38
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QY 39 SerGlnThrCysAlaSerAspTyrLeuLeuPhe-----ThrSerSerSerAsp 54
Db 549 AAGCATGACTGCAAGTATGACTTTCATTGAGATTCGGATGGAGACAGTGAAGTCAAGTGC 608
QY 55 GlnTyrGlyProTyrCysGlySerMetThrValProLysGluLeuLeuLeuAenThrSer 74
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Db 609 CTCCTGGGCAAGCACTGTGGGAACATT---GCCCTCCACCACATCATCTCTCTCCGGCTCC 665
QY 75 GluValThrValArgPheGluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThr 94
Db 666 GTGTTATATACAGTTTCACATCAGACTAGCCCGGCGAGGGGCGAGGTTTCTCCCTACGC 725
QY 95 Tyr-----AlaSerSerAsp----- 99
Db 726 TATGAGATCTTCAAAACAGGCTCTGAAGATTGTTCCAGAACTTTTACAAGCCCCCAATGGG 785
QY 100 -----HisProAspLeuIleThrCys----- 106
Db 786 ACATTGAATCTCCAGGGTTTCAGAGAAATATCCACAAATCTGGACTGTACCTTCACC 845
QY 107 ---LeuGluArgAlaSerHisIleLeuLeuLeuThrGluTyrSerLysPhe----- 121
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QY 122 -----CysProAlaGlyCysArgAspValAlaGlyAsp 132
Db 906 GACCTCTTACAAGTGGGGGAAGGAGACTGTAAATATGACTGGCTGGACATCTGGGATGC 965
QY 133 IleSer-----GlyAsnMetValAspGlyTyrArgAspThrSerLeuLeuCysLysAla 150
Db 966 ATTCCACATGTTGGGGCTCTGATTCGAAGTACTGTGGACGAGAAACACCCCTCCAAACTC 1025
QY 151 AlaIleHisAlaGlyIleIleAlaAspGluLeuGlyGlyGlnIleSerValLeuGlnArg 170
Db 1026 CGCTCGTCCACAGGATCTCTCCCTGACCTTTCACACGACATGGCCGCTGGCCAGGAT 1085
QY 171 LysGlyIleSerArgTyr-----GluGlyIleLeuAlaAsn 182
Db 1086 GCGCTTCTCAGCACGTTACTATTGTTGTCACCAAGAACCACTGAGAACTTTCAGTGCAT 1145
QY 183 GlyValLeuSerArgAsp---GlySerLeuSerAspLysArgPheLeuPheThrSerAsn 201
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QY 202 GlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerTyr 221
Db 1185 -----CAGATCAGTGCCTCATCCACCTTC 1208
QY 222 GlnSerValAsnGluSerGlyAspGlnValHisTyrProGlyGlnAlaArgLeuGln 241
Db 1209 -----TCTGATGGAGGTGGACTCTCTCAACAGCAGCAGGCTCCAT 1247
QY 242 AspGlnGlyProSerTyrPalaSerGlyAspSerSerAsnAsnHisLysProArgGluTyr 261
Db 1248 GGTGATGACAAATGGCTGGACACCCCAACGTTGGATTCCAAC-----AAGGATAT 1295
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QY 280 SerThrGlnSerAsnPheAsnPheValTyrValLysSerPheValMetAsnPheLysAsnAsn 299
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QY 360 CysGlnIleThrGlnGlyAsnAspSer-LeuValTyrArgLysThrSerGlnSerThrSe 379
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QY 379 rValSerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSe 399
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QY 399 r 399
Db 1689 t 1689
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US-08-936-135-17
; Sequence 17, Application US/08936135
; Patent No. 6054293
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: He, Zhigang
; TITLE OF INVENTION: Semaphorin Receptors
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,135
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC97-288-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2730 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-936-135-17
Alignment Scores:
Pred. No.: 1.72e-26 Length: 2730
Score: 329.50 Matches: 113
Percent Similarity: 40.79% Conservative: 73
Best Local Similarity: 24.78% Mismatches: 178
Query Match: 12.89% Indels: 92
Db: 3 Gaps: 18
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QY 21 ThrValProLys---GlyLysArgLeuIleLeuArgLeuGly---AspLeuAspIleGlu 38
Db 178 TAGCCCCCGGACCAACCAAGAGATTGCTCTCAACTCAACCCCTCACCTTTGAAATCGAG 237
QY 39 SerGlnThrCysAlaSerAspTyrLeuLeuPhe-----ThrSerSerSerAsp 54
Db 238 AAGCAGCAGTCAAGTATGACTTTATCGAGATTCCGGATTCGGGACAGTGAATCCCGCAG 297


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Db 595 GACCTTTTCAGCTGGAGAGGGGAGCTGCAAGTAGCTGGCTGGAGCATCTGGGATGGC 654
QY 133 IleSer-----GlyAsnMetValAspGlyTyrArgAspThrSerLeuLeuCysLysAla 150
Db 655 ATTCCACATGTTGGCCCTCGATTGGAAGTACTGTGGGACCAAAACACCTCTGAACCTT 714
QY 151 AlaIleHisAlaGlyIleAlaAspGluLeuGlyGlyGlnIleSerValLeuGlnArg 170
Db 715 CGTTCAATCAGCGGGATCTCTCCCTGAGCCTTTCAACGAGACATCGGCTGGCCAAAG--- 771
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Db 772 -----GATGGCTTCTCGCGCTTACTCTGTCTCCACCAAGAGCCA 813
QY 191 LeuSerAspLysArgPheLeuPheThrSerAsnGlyCysSerArgSerLeuSerPheGlu 210
Db 814 CTAGAGAACTTTTCAG-----TGCAATGTTCTCTGGCGCATGGAG 852
QY 211 -----ProAspGlyGlnIleArgAlaSerSerTyrPheGlnSerValAsnGlu 226
Db 853 TCTGGCCGATTCCTAATGAACAGATCAGTGCCTCATCTACCTAC----- 897
QY 227 SerGlyAspGlnValHisTyrSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSer 246
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Db 952 TGGACCCCAACTTGGATTTCCAAC-----AAGGAGTATCTCCAGGTGGACCTG 999
QY 267 GlyGluLysLysIleThrGlyIleArgThrThrGly-----SerThrGlnSerAsn 284
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QY 305 ThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsnSerAsnPheArg 324
Db 1120 GTGTACCGGCATGGCAAAACACAC-----AAGGTATTTCAAGCCCAACACATGCACT 1173
QY 325 AspProValGlnAsnAsnPheIleProPheValAlaArgTyrValArgValPro 344
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; Sequence 19, Application US/08936135
; Patent No. 6054293
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: He, Zhigang
; APPLICANT: Chen, Hang
; TITLE OF INVENTION: Semaphorin Receptors
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP
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STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT NUMBER: US/08/936,135
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC97-288-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 2781 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-936-135-19

Alignment Scores:
Pred. No.: 1-77e-26 Length: 2781
Score: 329.50 Matches: 113
Percent Similarity: 40.79% Conservatives: 73
Best Local Similarity: 24.78% Mismatches: 178
Query Match: 12.89% Indels: 92
DB: 3 Gaps: 18

US-10-813-588-2 (1-487) x US-08-936-135-19 (1-2781)
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Db 118 ATCACTCTCCCGTATACCCCGCAGGACTACCTCCACAGAACTGCGAGTGGATTGT 177
QY 21 ThrValProLys--GlyLysArgLeuIleLeuArgLeuGly--AspLeuAspIleGlu 38
Db 178 TAGCCCCCGAACCACCAAGAAATGTGCTCAACTCAACCTCACTTTGAAATCGAG 237
QY 39 SerGlnThrCysAlaSerAspTyrLeuLeuPhe-----ThrSerSerSerAsp 54
Db 238 AAGCAGCATTCGAATGATGACCTTTATCGAGATTCGGGATCGGACAGTGAATCCGACAG 297
QY 55 GlnTyrGlyProTyrCysGlySerMetThrValProLysGluLeuLeuLeuAsnThrSer 74
Db 298 CTCCTGGGCAACACTGTGGGAACATC---GCCCGCCGCCACCATCATCTCTCGGCTCC 354
QY 75 GluValThrValArgPheGluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThr 94
Db 355 ATGCTTACATCAAGTTCACTCCGACTACGCCCGCGGAGGGGCGAGGCTTCTCTCTGCGC 414
QY 95 Tyr-----AlaSerSerAsp----- 99
Db 415 TACGAGATCTTCAAGACAGGCTCTGAGATTCCTCAAAAACTTCAAGCCCCAACGGG 474
QY 100 -----HisProAspLeuIleThrCys----- 106
Db 475 ACCATCGAATCTCTGGGTTTCTCGAAGAGTATCCACAACTTGGACTGCACCTTTTACC 534
QY 107 ---LeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLysPhe----- 121
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QY 122 -----CysProAlaGlyCysArgAspValAlaGlyAsp 132
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Db      595  GACCCCTTTCAGGTGGAGAGGGGACTGCAAGTACGATTGGCTGGACATCTGGGATGGC 654
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Db      655  ATTCCACATGTTGGCCCCCTGATTGGCAAGTACTGTGGGACCAAAACACCCCTCTGAAC TT 714
Qy      151  AlaIleHisAlaGlyIleIleAlaAspGluLeuGlyGlyGlnIleSerValLeuGlnArg 170
Db      715  CGTTTCATCGACGGGGATCTCTCCCTGACCTTTCCACGCGACATGGCGGTGGCCAAG--- 771
Qy      171  LysGlyIleSerArgTyrGluGlyIleLeuAlaAsnGlyValLeuSerArgAspGlySer 190
Db      772  -----GATGGCTTCTCTGGCGGTACTACTCTGTCCCAAGAGCCCA 813
Qy      191  LeuSerAspIysArgPheLeuPheThrSerAsnGlyCysSerArgSerLeuSerPheGlu 210
Db      814  CTAGAGAACTTTCAG-----TGCAATGTTCTCTGGGCATGGAG 852
Qy      211  -----ProAspGlyGlnIleArgAlaSerSerSerTrpGlnSerValAsnGlu 226
Db      853  TCTGGCCGGATTGCTAATGAACAGATCAGTGCCTCATCTACTACTAC----- 897
Qy      227  SerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSer 246
Db      898  -----TCTGATGGGAGGTGGACCCCTCAACAAGCGCGCTCCATGGTGATGACAATGGC 951
Qy      247  TrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGluTrpLeuGluIleAspLeu 266
Db      952  TGGACCCCAACTTGGATCCAC-----AGGAGTATCTCCAGGTGGACCTG 999
Qy      267  GlyGluLysLysLysIleThrGlyIleArgThrGly-----SerThrGlnSerAsn 284
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Qy      285  PheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsnSerLysTrpLys 304
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Qy      305  ThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsnSerAsnPheArg 324
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Qy      325  AspProValGlnAsnAsnPheIleProPheIleValAlaArgTyrValArgValPro 344
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Qy      345  GlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCysGlnIleThrGln 364
Db      1234  CAGACCTGGCACTCAGGTATCGCCCTCCGGCTGGAGCTCTTCGGCTGCCGGGTACAGAT 1293
Qy      365  GlyAsnAspSer-LeuValTrpArgLysThrSerGlnSerThrSerValSerThrLysLy 384
Db      1294  GCTCCCTGCTCCAAACATGCTGG-----GGATGCTCTCAGGCCTCATTTGCAGACTCCCAG 1347
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Search completed: January 15, 2006, 23:07:32
Job time : 278 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2006, 20:06:18 ; Search time 387 Seconds
(without alignments)
1018.482 Million cell updates/sec

Title: US-10-813-588-2

Perfect score: 2557

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
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Searched: 6038814 seqs, 404674181 residues

Total number of hits satisfying chosen parameters: 12077628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

Published Applications NA New.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	285.5	11.2	1400	7	US-11-128-061-3655
5	285.5	11.2	4374	7	US-11-128-061-13
6	285.5	11.2	4999	6	US-10-632-645-14
7	285.5	11.2	11933	6	US-10-632-645-13
8	280	11.0	452	7	US-11-136-527-989

9	280	11.0	452	7	US-11-136-527-5085
10	217	8.5	3935	6	US-10-947-249-162
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ALIGNMENTS

RESULT 1

US-11-136-527-2829
; Sequence 2829, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2829
; LENGTH: 3371
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2829

Alignment Scores:	1.46e-25	Length:	3371
Pred. No.:	331.50	Matches:	112
Score:	40.13%	Conservative:	73
Best Local Similarity:	24.30%	Mismatches:	174
Query Match:	12.96%	Indels:	102
DB:	7	Gaps:	17

US-10-813-588-2 (1-487) x US-11-136-527-2829 (1-3371)

QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20

429	Db	ATC	ACTTCC	CCAGGTTACCC	CCAGGATATCCCTCTCACCAGAACTGTGAGTGGGTGTC	488																	
21	Qy	Thr	Val	Pro	Lys---Gly	LysArgLeuLleuArgLeuGly---Asp	LeuAspLleuGlu	38															
489	Db	TAT	GCCCCC	CAACCCAA	CCAGAGATGTCTCAACTTCAACCTCACCTTTGAAATCGAG	548																	
39	Qy	Ser	Gln	Thr	Cys	Ala	SerAspTyr	LeuLeuPhe-----Thr	SerSerAsp	54													
549	Db	AAG	CATGAC	TGCAAGTATGAC	TTCATTGAGATTCCGGATGCGAGACGAGTGCAGCTGAC	608																	
55	Qy	Gln	Tyr	Gly	Pro	Tyr	CysGlySerMet	ThrVal	ProLysGluLeuLeuLeuAsn	ThrSer	74												
609	Db	CTC	CTGGCA	AGCACTGTGGGAACAT	T---GCCCTCCCAACCATCATCTCTTCGCGCTCC	665																	
75	Qy	Glu	Val	Thr	Val	Arg	Phe	Glu	SerGlySerHis	LeuArgGlyPheLeuLeu	Thr	94											
666	Db	GTG	TATATAT	CAAGTTTCA	CATCAGATACGCGCGG	CAGGGGAGGTTTCTCCCTACGC	725																
95	Qy	Tyr	---	---	Ala	Ser	SerAsp	---	---	---	---	99											
726	Db	TAT	GAGATCTT	CAAAACAGGCTCTG	AGATTGTTCCAAAGAACTTACAACGCCCAATGGG	785																	
100	Qy	---	---	---	---	---	---	---	His	Pro	Asp	Leu	Leu	Thr	Cys	---	106						
786	Db	ACC	ATTGAA	TCTCCAGG	GTTTCCAGAGAAATATCCACACAATCTGGACTGTACTCTCAC	845																	
107	Qy	---	---	Leu	Glu	Arg	Ala	Ser	His	Tyr	Leu	Leu	Thr	Clu	Tyr	Ser	Lys	Phe	---	121			
846	Db	ATC	CTGGCC	CAAAACCC	AGATGGAGATCATCTACAGTCTCTGACCTTTGACCTGGAGCAT	905																	
122	Qy	---	---	---	---	---	---	---	Cys	Pro	Ala	Gly	Cys	Arg	Asp	Val	Ala	Gly	Asp	132			
906	Db	GAC	CTCTA	CAAGTGGG	GAAGAGACTGTAAATATGACTGGCTGGACATCTGGGATGGC	965																	
133	Qy	I	le	Ser	---	---	Gly	Asn	Met	Val	Asp	Gly	Tyr	Arg	Asp	Thr	Ser	Leu	Leu	Cys	Leu	Ala	150
966	Db	ATT	CCACAT	GTTGGG	CCCTCTGATTGGCAAGTACTGTGGACGAAACACACCTCTCCAACTC	1025																	
151	Qy	Ala	le	His	Ala	Gly	Ile	le	Ala	Asp	Clu	Leu	Gly	Gly	Gln	Ile	Ser	Val	Leu	Gln	Arg	170	
1026	Db	CGC	TCGT	CCACAGGAT	CTCTCCCTGACCTTTCCACCGGACATGGCGGTGGCCAGGAT	1085																	
171	Qy	Lys	Gly	Ile	Ser	Arg	Tyr	---	---	---	---	---	---	---	---	Glu	Gly	Ile	Leu	Ala	Asn	182	
1086	Db	GGC	TTCTCAG	CACGCTTACTATT	TGGTCCACCAAGAACCACTGAGAACTTTCAGTGCAT	1145																	
183	Qy	Gly	Val	Leu	Ser	Arg	Asp	---	---	Gly	Ser	Leu	Ser	Asp	Lys	Arg	Phe	Leu	Phe	Thr	Ser	Asn	201
1146	Db	GCC	CTCTGG	CAATGGAGTCTG	CGCGGATTGCTAATGAA-----	1184																	
202	Qy	Gly	Cys	Ser	Arg	Ser	Leu	Ser	Phe	Clu	Pro	Asp	Gly	Gln	Ile	Arg	Ala	Ser	Ser	Ser	Tyr	221	
1185	Db	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1208	
222	Qy	Gln	Ser	Val	Asn	Glu	Ser	Gly	Asp	Gln	Val	His	Tyr	Ser	Pro	Gly	Gln	Ala	Arg	Leu	Gln	241	
1209	Db	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1247	
242	Qy	Asp	Gln	Gly	Pro	Ser	Trip	Ala	Ser	Gly	Asp	Ser	Ser	Asn	Asn	His	Lys	Pro	Arg	Glu	Tyr	261	
1248	Db	GGT	GATG	CAATGG	CTGGAC	CCCAACCGTGGATTCCAAC-----AAG	GATAT	1295															
262	Qy	Leu	Glu	Ile	Asp	Leu	Gly	Glu	Lys	Lys	Ile	Thr	Gly	Ile	Arg	Thr	Thr	Gly	---	---	---	279	
1296	Db	CTC	CAGGTGG	AGCTCG	CGCTCTCC	TACCACTGTCTCAGAGCCATTGCAAC	CAAGAGCCATT	1355															
280	Qy	Ser	Thr	Gln	Ser	Asn	Phe	Asn	Phe	Tyr	Val	Lys	Ser	Phe	Val	Met	Asn	Phe	Lys	Asn	Asn	299	
1356	Db	TCC	AGGG	AGACCC	GAAGGGCTACTAC	TGCTCAATCGTAAAGCTGGAGTGCAGCAAC	1415																
300	Qy	Asn	Ser	Lys	Trip	Lys	Thr	Tyr	Lys	Thr	Val	Asn	Asn	Glu	Glu	Lys	Val	Phe	Gln	Gly	319		


```
QY 397 luThrSerThrGlyLeuAenlleThrThrValalaileProLeu 411
||||| ||||| ||||| ||||| ||||| |||||
Db 1503 AGACAGGAAGTGGATGCCAGAAACATCGCCTGGTGACCACTG 1546

RESULT 4
US-11-128-061-3655
; Sequence 3655, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; PRIOR FILING DATE: 2005-05-11
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3655
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-128-061-3655

Alignment Scores:
Pred. No.: 5,02e-21 Length: 1400
Score: 285.50 Matches: 62
Percent Similarity: 56.97% Conservative: 32
Best Local Similarity: 37.58% Mismatches: 58
Query Match: 11.17% Indels: 13
DB: 7 Gaps: 4

US-10-813-588-2 (1-487) x US-11-128-061-3655 (1-1400)
QY 201 AsnGlyCysSerArgSerLeuSerPheGlu-----ProAspGlyGlnIleArg 216
||||| ||||| ||||| ||||| ||||| |||||
Db 915 AATAGTTGCAGCATGCCATTGGGAATGGAGATAAGCAATATCAGATGCACAGATTACT 974

QY 217 AlaSerSerSerTrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGly 236
||||| ||||| ||||| ||||| ||||| |||||
Db 975 GCTTCATCTCTACTTTACCAATATGTTGCCACC-----TGGTCTCTCTCA 1019

QY 237 GlnAlaArgLeuGlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHis 256
||||| ||||| ||||| ||||| ||||| |||||
Db 1020 AAAGCTCGACTTCACCTCCAGGAGGAGTAAATGCTGGAGACCTCAGGTGAATAT- 1076

QY 257 LysProArgGluTrpLeuGluIleAspLeuGlyLysLysLysLysLysLysLysLysLys 276
||||| ||||| ||||| ||||| ||||| |||||
Db 1077 ---CCAAAAGAGTGGCTGCAAGTGGACTTCCAGAGACAATGAAGTCAAGAGTAAC 1133

QY 277 ThrThrGlySerThrGlnSerAsnPheAsnPheThrValLysSerPheValMetAsnPhe 296
||||| ||||| ||||| ||||| ||||| |||||
Db 1134 ACTCAGGAGTAAATCTCTGCTTACCAGCATGTATGTGAAGGAGTTCTCTCATCTCCAGC 1193

QY 297 LysAsnAsnAsnSerLysTrpLysThrLysGlyIleValAsnAsnGluLysVal 316
||||| ||||| ||||| ||||| ||||| |||||
Db 1194 AGTCAAGATGGCATCAGTGGACTCTCTT-----TTTCAGATGGCAAGTAAGGTT 1247

QY 317 PheGlnGlyAsnSerAsnPheArgProValGlnAsnAsnPheIleProIleVal 336
||||| ||||| ||||| ||||| ||||| |||||
Db 1248 TTTCAGGGAATCAAGACTCTTCCACACCTGTGGTGAATCTCTAGACCCACCGTTACTG 1307

QY 337 AlaArgTyrValArgValProGlnThrTrpHisGlnArgIleAlaLeuLysValGlu 356
||||| ||||| ||||| ||||| ||||| |||||
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```
Db 1308 ACTGCTACCTTCGAATTCACCCAGAGTTGGGTGCACAGATTGCCCTGAGGATGGAG 1367
QY 357 LeuIleGlyCysGln 361
||||| ||||| ||||| ||||| ||||| |||||
Db 1368 GTTCTGGGCTGGAG 1382

RESULT 5
US-11-128-061-13
; Sequence 13, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; PRIOR FILING DATE: 2005-05-11
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 4374
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-128-061-13

Alignment Scores:
Pred. No.: 3e-20 Length: 4374
Score: 285.50 Matches: 62
Percent Similarity: 56.97% Conservative: 32
Best Local Similarity: 37.58% Mismatches: 58
Query Match: 11.17% Indels: 13
DB: 7 Gaps: 4

US-10-813-588-2 (1-487) x US-11-128-061-13 (1-4374)
QY 201 AsnGlyCysSerArgSerLeuSerPheGlu-----ProAspGlyGlnIleArg 216
||||| ||||| ||||| ||||| ||||| |||||
Db 3889 AATAGTTGCAGCATGCCATTGGGAATGGAGATAAGCAATATCAGATGCACAGATTACT 3948

QY 217 AlaSerSerSerTrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGly 236
||||| ||||| ||||| ||||| ||||| |||||
Db 3949 GCTTCATCTCTACTTTACCAATATGTTGCCACC-----TGGTCTCTCTCA 3993

QY 237 GlnAlaArgLeuGlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHis 256
||||| ||||| ||||| ||||| ||||| |||||
Db 3994 AAAGCTCGACTTCACCTCCAGGAGGAGTAAATGCTGGAGACCTCAGGTGAATAT- 4050

QY 257 LysProArgGluTrpLeuGluIleAspLeuGlyLysLysLysLysLysLysLysLysLys 276
||||| ||||| ||||| ||||| ||||| |||||
Db 4051 ---CCAAAAGAGTGGCTGCAAGTGGACTTCCAGAGACAATGAAGTCAAGAGTAAC 4107

QY 277 ThrThrGlySerThrGlnSerAsnPheAsnPheThrValLysSerPheValMetAsnPhe 296
||||| ||||| ||||| ||||| ||||| |||||
Db 4108 ACTCAGGAGTAAATCTCTGCTTACCAGCATGTATGTGAAGGAGTTCTCTCATCTCCAGC 4167

QY 297 LysAsnAsnAsnSerLysTrpLysThrLysGlyIleValAsnAsnGluLysVal 316
||||| ||||| ||||| ||||| ||||| |||||
Db 4168 AGTCAAGATGGCATCAGTGGACTCTCTT-----TTTCAGATGGCAAGTAAGGTT 4221

QY 317 PheGlnGlyAsnSerAsnPheArgProValGlnAsnAsnPheIleProIleVal 336
||||| ||||| ||||| ||||| ||||| |||||
Db 4222 TTTCAGGGAATCAAGACTCTTCCACACCTGTGGTGAATCTCTAGACCCACCGTTACTG 4281

QY 337 AlaArgTyrValArgValProGlnThrTrpHisGlnArgIleAlaLeuLysValGlu 356
||||| ||||| ||||| ||||| ||||| |||||
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Db 4282 ACTCGCTACCTTCGAATTCACCCACAGATTGGTGCCAGATTGCCCTCAGGATGGAG 4341
Qy 357 LeuIleGlyCysGln 361
Db 4342 GTTCTGGGCTCGGAG 4356

RESULT 6
US-10-632-645-14
; Sequence 14, Application US/10632645
; Publication No. US20050276787A1
; GENERAL INFORMATION:
; APPLICANT: Couto, Linda B.
; APPLICANT: Colosi, Peter C.
; TITLE OF INVENTION: Adeno-Associated Vectors for Expression of Factor VIII
; TITLE OF INVENTION: by Target Cells
; FILE REFERENCE: Avigen-04082
; CURRENT APPLICATION NUMBER: US/10/632,645
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/740,211
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/470,618
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/125,974
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/104,994
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 4999
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-632-645-14

Db 4637 TTTTCAGGGAATCAAGACTCTTTCACACCCTGTGGTGAACTCTCTAGACCCACCACCGTTACTG 4696

Qy 337 AlaArgTyRValArgValProGlnInThrTrpHisGlnArgIleAlaLeuLysValGlu 356
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 4697 ACTCGCTACTCTCGAATTCCACCCCAGAGTTGGGTGCACACAGATTGCCCTGAGGATGGAG 4756

Qy 357 LeuIleGlyCysGln 361
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

Db 4757 GTTCTGGGCTCGAG 4771

RESULT 7

US-10-632-645-13

; Sequence 13, Application US/10632645

; Publication No. US20050276787A1

; GENERAL INFORMATION:

; APPLICANT: Couto, Linda B.

; APPLICANT: Colosi, Peter C.

; TITLE OF INVENTION: Adeno-Associated Vectors for Expression of Factor VIII

; TITLE OF INVENTION: by Target Cells

; FILE REFERENCE: Avigen-04082

; CURRENT APPLICATION NUMBER: US/10/632,645

; CURRENT FILING DATE: 2003-08-01

; PRIOR APPLICATION NUMBER: US/09/740,211

; PRIOR FILING DATE: 2000-12-18

; PRIOR APPLICATION NUMBER: 09/470,618

; PRIOR FILING DATE: 1999-12-22

; PRIOR APPLICATION NUMBER: 60/125,974

; PRIOR FILING DATE: 1999-03-24

; PRIOR APPLICATION NUMBER: 60/104,994

; PRIOR FILING DATE: 1998-10-20

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 13

; LENGTH: 11933

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-632-645-13

Alignment Scores:

Pred. No.: 1,45e-19 Length: 11933

Score: 285.50 Matches: 62

Percent Similarity: 56.97% Conservative: 32

Best Local Similarity: 37.58% Mismatches: 58

Query Match: 11.17% Indels: 13

DB: Gaps: 4

US-10-813-588-2 (1-487) x US-10-632-645-13 (1-11933)

Qy 201 AsnGlyCysSerArgSerLeuSerPheGlu-----ProAspGlyGlnIleArg 216
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

Db 4279 AATAGTTGCAGCATGCCATTGGGAATGGAGATAAGCAATATCATGATCACAGATTACT 4338

Qy 217 AlaSerSerSerTrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGly 236
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

Db 4339 GCCTTCATCTACTTTTACCAATATGTTTGCACC-----TGGTCTCTCTCA 4383

Qy 237 GlnAlaArgLeuGlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHis 256
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

Db 4384 AAAGCTCGACTTTCACCTCCAAGGGAGAGTAATGCTGGAGACCTCAGGTTGAATAAT--- 4440

Qy 257 LysProArgGluTrpLeuGlnIleAspLeuGlyGluLysIleThrGlyIleArg 276
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

Db 4441 ---CCAAAAGAGTGGCTCGAAGTGGACTTCCAGAAGACAATGAAGATCACAGGATTA 4497

Qy 277 ThrThrGlySerThrGlnSerAsnPheAsnPheTyRValLysSerPheValMetAsnPhe 296
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

Db 4498 ACTCAGGGAGTAAAACTCTGCTTACCAGCATCTATGTGAAGAGTTCCTCATCTCCAGC 4557

Qy 297 LysAsnAsnAsnSerLysTrpLysThrTyRlysGlyIleValAsnAsnGluGlutylVal 316
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

Db 4558 AGTCAAGATGGCCCATCAGTGGACTCTCTTT-----TTTCAGAAATGCAAAGTAAAGGTT 4611

QY 317 PheGlnGlyAsnSerAsnPheArgAspProValGlnAsnAsnPheIleProProIleVal 336
 ||||| ||||| : : : ||||| ||||| : : : ||||| : : : ||||| : : :
 Db 4612 TTTTACGGGAAATCAAGACTCTTCCACACCTGTGGTGAATCTCTAGACCCACCGTTACTG 4671

QY 337 AlaArgTyrValArgValProGlnThrTrpHisGlnArgIleAlaLeuLysValGlu 356
 ||||| ||||| : : : ||||| ||||| : : : ||||| ||||| : : : ||||| : : : ||||| : : :
 Db 4672 ACTCGCTACTCTCGAATTACCCCCAGAGTTGGTGCCACAGATTGCCCTGAGGATGGAG 4731

QY 357 LeuIleGlyCysGln 361
 :
 Db 4732 GTTCTGGGCTGGAG 4746

RESULT 8

US-11-136-527-989/c
 ; Sequence 989, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; CURRENT FILING DATE: 2005-05-25
 ; PRIOR APPLICATION NUMBER: US 60/574,294
 ; PRIOR FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362830
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 989
 ; LENGTH: 452
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 US-11-136-527-989

Alignment Scores:
 Pred. No.: 3.5e-21 Length: 452
 Score: 280.00 Matches: 54
 Percent Similarity: 63.36% Conservative: 29
 Best Local Similarity: 41.22% Mismatches: 46
 Query Match: 10.95% Indels: 2
 DB: 7 Gaps: 1

US-10-813-588-2 (1-487) x US-11-136-527-989 (1-452)

QY 232 HisTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSerTrpAlaSerGlyAsp 251
 :
 Db 425 TACTGGGAGCCTTCCCTTGGCCGCTGAATGCCAGGCCGAGTGAATGCTTGGCAAGCC 366

QY 252 SerSerAsnAsnHisLysProArgGluTrpLeuGluIleAspLeuGlyGluLysLysLys 271
 :
 Db 365 AAGGCAACCAACAACAG-----CAGTGGTTACAAATTGATCTGCTCAAAATCAAGAAG 312

QY 272 IleThrGlyIleArgThrThrGlySerThrGlnSerAsnPheAsnPheTyrValLysSer 291
 :
 Db 311 GTAACGGCCATCGTAACCTAGGTTGCAGTCTCTGCTGAGATGATGTGAAGAGC 252

QY 292 PheValMetAsnPheLysAsnAsnSerLysTrpLysThrTyrLysGlyIleValAsn 311
 :
 Db 251 TACAGCATCTCTGTCAGTGACCGGGGTCTCTCTGGAAACCCCTACCGGAGAAATCTCTCC 192

QY 312 AsnGluGluLysValPheGlnGlyAsnSerAsnPheArgAspProValGlnAsnAsnPhe 331
 :
 Db 191 ATGGTGACCAAGATTTTGAAGGGAATAGCAATACCAAGGGCATATGAAGAATCTTTTC 132

QY 332 IleProIleValAlaArgTyrValArgValProGlnThrTrpHisGlnArgIle 351
 :
 Db 131 AACCCACTATTATTCCAGATTATCCGAATCTCTTAAACGTTGAACCAAAAGTATT 72

QY 352 AlaLeuLysValGluLeuIleGlyCysGlnIle 362
 :
 Db 71 GCACCTTCGCTGGAACCTCTTCGGCTGTGACATT 39

RESULT 9

US-11-136-527-5085
 ; Sequence 5085, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; CURRENT FILING DATE: 2005-05-25
 ; PRIOR APPLICATION NUMBER: US 60/574,294
 ; PRIOR FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362830
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 5085
 ; LENGTH: 452
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 US-11-136-527-5085

Alignment Scores:
 Pred. No.: 3.5e-21 Length: 452
 Score: 280.00 Matches: 54
 Percent Similarity: 63.36% Conservative: 29
 Best Local Similarity: 41.22% Mismatches: 46
 Query Match: 10.95% Indels: 2
 DB: 7 Gaps: 1

US-10-813-588-2 (1-487) x US-11-136-527-5085 (1-452)

QY 232 HisTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSerTrpAlaSerGlyAsp 251
 :
 Db 28 TACTGGGAGCCTTCCCTTGGCCGCTGAATGCCAGGCCGAGTGAATGCTTGGCAAGCC 87

QY 252 SerSerAsnAsnHisLysProArgGluTrpLeuGluIleAspLeuGlyGluLysLysLys 271
 :
 Db 88 AAGGCAACCAACAACAG-----CAGTGGTTACAAATTGATCTGCTCAAAATCAAGAAG 141

QY 272 IleThrGlyIleArgThrThrGlySerThrGlnSerAsnPheAsnPheTyrValLysSer 291
 :
 Db 142 GTAACGGCCATCGTAACCTAGGTTGCAGTCTCTGCTGAGATGATGTGAAGAGC 201

QY 292 PheValMetAsnPheLysAsnAsnSerLysTrpLysThrTyrLysGlyIleValAsn 311
 :
 Db 202 TACAGCATCTCTGTCAGTGACCGGGGTCTCTCTGGAAACCCCTACCGGAGAAATCTCTCC 261

QY 312 AsnGluGluLysValPheGlnGlyAsnSerAsnPheArgAspProValGlnAsnAsnPhe 331
 :
 Db 262 ATGGTGACCAAGATTTTGAAGGGAATAGCAATACCAAGGGCATATGAAGAATCTTTTC 321

QY 332 IleProIleValAlaArgTyrValArgValProGlnThrTrpHisGlnArgIle 351
 :
 Db 322 AACCCACTATTATTCCAGATTATCCGAATCTCTTAAACGTTGAACCAAAAGTATT 381

QY 352 AlaLeuLysValGluLeuIleGlyCysGlnIle 362
 :
 Db 382 GCACCTTCGCTGGAACCTCTTCGGCTGTGACATT 414

RESULT 10

US-10-947-249-162
 ; Sequence 162, Application US/10947249
 ; Publication No. US20050287541A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Akira NAKAGAWARA
 ; APPLICANT: Miki OHIRA
 ; APPLICANT: Shin ISHII
 ; APPLICANT: Takeshi GOTO
 ; APPLICANT: Hiroyuki KUBO
 ; APPLICANT: Takahiro HIRATA
 ; APPLICANT: Yasuko YOSHIDA
 ; APPLICANT: Saichi YAMADA
 ; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma and Met
 ; PREDICTING THE PROGNOSIS OF NEUROBLASTOMA

```
FILE REFERENCE: 117007
CURRENT APPLICATION NUMBER: US/10/947,249
CURRENT FILING DATE: 2004-09-23
PRIOR APPLICATION NUMBER: 2004-09-23
PRIOR APPLICATION NUMBER: US 60/505,614
PRIOR APPLICATION NUMBER: 2003-09-25
NUMBER OF SEQ ID NOS: 200
SOFTWARE: PatentIn version 3.1
SEQ ID NO 162
LENGTH: 3935
TYPE: DNA
ORGANISM: Homo sapiens
US-10-947-249-162

Alignment Scores:
Pred. No.: 1,13e-12 Length: 3935
Score: 217.00 Matches: 55
Percent Similarity: 44.39% Conservative: 40
Best Local Similarity: 25.70% Mismatches: 97
Query Match: 8.49% Indels: 22
DB: 6 Gaps: 5

US-10-813-588-2 (1-487) x US-10-947-249-162 (1-3935)
QY 212 AspGlyGlnIleArgAlaSerSerTrpGln---SerValAsnGluSerGlyAspGln 230
DB 1328 GACAACACAGATCGAGCTCTCCATGCTGGCCGCGCTGGGGGCACAGCGCGCGG 1387
QY 231 ValHisTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSerTrpAlaSerGly 250
DB 1388 CTCACATGACGACCGGCTCCACTGAGGACGACTACTATGATGGTGGTGGTGGCCGAG 1447
QY 251 AspSerSerAsnAsnHisLysProArgGluTrpLeuGluIleAspLeuGlyGluLysLys 270
DB 1448 GACGATGCCAGGACC-----CAGTGGATAGAGTGGACACACAGGAGGACTACC 1495
QY 271 LysIleThrGlyIleArgThrThrGlySerThrGlnSerAsnPheAsnPheTrpValLys 290
DB 1496 CGGTTTCACAGGCGTCTATCACCAGGCGAGACTCCAGCATCCATGACGATTTGTGACC 1555
QY 291 SerPheValMetAsnPheLysAsnAsnSerLysTrpLysThrTrpLysGlyIleVal 310
DB 1556 ACCTTCTTCGTGGGCTTCAGCAATGACACGACATGGGTGATGTATACACCAAC----- 1609
QY 311 AsnAsnGluLysValPheGlnGlyAsnSerAsnPheArgAspProValGlnAsnAsn 330
DB 1610 GCCTATGAGGAATGACCTTTCATGGACAGTGGACAGGACACACCCGCTGTGAGTGAG 1669
QY 331 PheIleProProIleValAlaArgTyrValArgValProGlnThrTrpHisGlnArg 350
DB 1670 CTCACAGAGCGGTGGTGGTCTGTTTCATCCGATCTACCCACTCCTGGAATGGCAGC 1729
QY 351 IleAlaLeuLysValGluLeuIleGlyCysGlnIleThrGln----- 364
DB 1730 CTGTGATCGGCTGGAGTGTGGGGTCTCTGTGGCCCTCTCTACAGCTACTACGCA 1789
QY 365 -----GlyAsnAspSerLeuValTrpArg-----LysThrSer 375
DB 1790 CAGATAGGTGGTGGCCACCATGACCTGGATTTCGGCACACACAGCTACAGGACATG 1849
QY 376 GlnSerThrSerValSerThrLysLysGluAspGluThrIleThrArgProIleProSer 395
DB 1850 CGCCAGCTCATGAAGGTGGTGAACAGGAGTGGCCACCATCACCAGCATTTACAGCCTG 1909
QY 396 GluGluThrSerThrGlyIleAsnIleThrThrValAlaIle 409
DB 1910 GCAAGAGCTCAGAGGCGCTCAAGATCTATGCCATGGAGATC 1951

RESULT 11
US-10-131-826A-391
; Sequence 391, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
```

```
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330RIC128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 391
LENGTH: 3772
TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-826A-391

Alignment Scores:
Pred. No.: 4,47e-09 Length: 3772
Score: 184.50 Matches: 72
Percent Similarity: 42.81% Conservative: 47
Best Local Similarity: 25.90% Mismatches: 105
Query Match: 7.22% Indels: 55
DB: 6 Gaps: 12

US-10-813-588-2 (1-487) x US-10-131-826A-391 (1-3772)
QY 130 AlaGlyAspIleSerGlyAsnMetVal-----AspGlyTyrArgAspThrSerLeu 146
DB 436 GCAGGAGATCTGGAGCCCGGAGCCCTACTACTACGCGCGCGGAGCGCGGAGTTCGAGACCTT 495
QY 147 LeuCysLysAlaAlaIleHisAla-----GlyIleIleAlaAspGluLeuGlyGln 164
DB 496 CTCCTCCGCGCTGCTGGCGGCGCGGAGGAGTGGGAGCGCGCGCGCGCGCGCGCGCG 555
QY 165 IleSerValLeuGlnArgLysGly-----IleSerArgTyrGluGlyIleLeu 180
DB 556 GCCGCC-----CAAGAGGCGCCACAGCCCAAGAAAGCTCCCAAGAGGAGGAGATC 606
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
```

Db 607 GGCTCGGAGCGCCCTCCA--CCAGGTAAACACAGCAACAAAAAGTTATGAGAACCAAG 664
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
Db 665 -----AGCTCTGAGAAGGCTGCCAACGATGATCAGAGTGTGCGTGGCCCGT--- 712
QY 221 TrpGlnSerValAsnGluSer-----Gly 228
Db 713 --GAAGATGTCAGAGAGAGTTGCCACCCTCTTGGTCTGGAAACCTTAAAAATCAGAC 769
QY 229 AspGlnValHisTrpSer-----ProGlyGlnAlaArgLeu 240
Db 770 TTCACGCTCCATCGCTCCACGGTGAAGCGCTATGGCTGGGGGCACATCGGGGAGACTC 829
QY 241 GlnAspGlnGly-----ProSerTrpAlaSerGlyAsp 251
Db 830 AACATCCAGCGCGGCATTAAATGAATGATTTTATGACGGAGCGTGGTGGCGGGA--- 886
QY 252 SerSerAsnAsnHisLysProArgGluTrpLeuGluIleAspLeuGlyGlnLysLys 271
Db 887 -----AGAAATGACCTCCACGACAGTGTGAAGTGAATGCTCGGGCGCTGACACAGA 937
QY 272 IleThrGlyIleArgThrGlySerThrGlnSerAsnPheAsnPheTyrValLysSer 291
Db 938 TTCACGTGGTGTATCACTCAAGGGAGGAACCTCCCTCTGGCTGAGTGACTGGGTGACATCC 997
QY 292 PheValMetAsnPheLysAsnAsnAsnSerLysTrpLysGlyIleValAsn 311
Db 998 TATAAGGTCAATGGTGAGCAATGACACACACCTGGTCACTGTTAAGAAAT-----GGA 1051
QY 312 AsnGluGluLysValPheGlnGlyAsnSerAsnPheArgAspProValGlnAsnAsnPhe 331
Db 1052 TCTGGAGCATGATATTTCAGGGAAACAGTGAAGAGGAGATCCCTGTCTCAATGAGCTA 1111
QY 332 IleProProIleValAlaArgTyrValArgValValProGlnThrTrpHisGlnArg--- 350
Db 1112 CCGTCCCATGGTGGCCGCTACATCCGCATAAACCTCAGTCCGTGGTGGTATGATGGG 1171
QY 351 ---IleAlaLeuLysValGluIleGlyCysGlnIleThrGlnGlyAsnAsp 367
Db 1172 AGCATCTGCATGAGATGGAGATCCTGGGCTGCCCATGCCAGATCCTAATAAT 1225

RESULT 12

US-11-137-465-32
; Sequence 32, Application US/11137465
; Publication No. US2005025558A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safie, K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kohnick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
; CURRENT APPLICATION NUMBER: US/11/137,465
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/239,663
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 2205
; TYPE: DNA
; ORGANISM: Homo sapiens

US-11-137-465-32

Alignment Scores:
Pred. No.: 2,866-08 Length: 2205
Score: 174.00 Matches: 64
Percent Similarity: 42.86% Conservative: 32
Best Local Similarity: 28.57% Mismatches: 84
Query Match: 6.80% Indels: 47
DB: 7 Gaps: 5
US-10-813-588-2 (1-487) x US-11-137-465-32 (1-2205)
QY 212 AspGlyGlnIleArgAlaSerSerSerTrp----- 221
Db 379 GATAGCCGCTTGGAGCATCCAGCAGCCAGTCTTTGGTCTTGGACCACACCGAGACGG 438
QY 222 -----GlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAla 238
Db 439 CTCACATTCATCAGGCTGGAGGAGCGGATCT-ATATGATGGAG-CTTGGTGTGCTG 496
QY 239 ArgLeuGlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysPro 258
Db 497 AGGAG-CAGGACGCCGATCCA----- 516
QY 259 ArgGluTrpLeuGluIleAspLeuGlyGlnLysLysLysIleThrGlyIleArgThrThr 278
Db 517 -----TGGTTTCAGGTGGACCTGGGCAACCCACCCGCTTCTCGGGTGTATCAGACAG 570
QY 279 GlySerThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsn 298
Db 571 GCGAGAACTCTGTCTGGAGGTATGACTGGGTACATCATACAGTCCAGTTCAGCAAT 630
QY 299 AsnAsnSerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGln 318
Db 631 GACAGTCGACCTGGTGGGGAAGTGAACACACAGCAGTGGATGGACGCAAGTATTTCTCT 690
QY 319 GlyAsnSerAsnPheArgAspProValGlnAsnAsnPheIleProIleValAlaArg 338
Db 691 GCAATTCAGACCCAGAAATCCAGTGTGAACCTCTCCCGAGAGCCCGAGTGGCCCGC 750
QY 339 TyrValArgValValProGlnThrTrpHisGlnArgIleAla-----LeuLysValGlu 356
Db 751 TTCAATTCGCTGCTGCCACGACCTGGCTCCAGGAGGCGCGCTTGGCTCCGGGCGAG 810
QY 357 LeuIleGlyCysGlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGln 376
Db 811 ATCTGGCTGCCAGTCTCAGACCCCAATGACCTATTCTTGGAGGCCCTGCGTGGGA 870
QY 377 SerThr-SerValSerThrLysLysGluAspGluThrIleThrArgPro----- 392
Db 871 TCTCTGACCTCTAGACT-----TTCAGCATCAATTTACAGGCCCATGAGGAAGCTG 924
QY 393 -----IleProSerGluGluThrSerThrGlyIleAsnIleTh 405
Db 925 ATGAACGAGGTACAGACGAATGCCCAACATCACCCGCATCTACAGCATTTGGGAAGAGC 984
QY 405 rThrValAla 408
Db 985 TACCAGGGCC 994

RESULT 13

US-10-852-893-1
; Sequence 1, Application US/10652893
; Publication No. US2005024973A1
; GENERAL INFORMATION:
; APPLICANT: Balasubramanian, Sriam
; APPLICANT: Ford, John
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MAMMALIAN PROTEASES; RELATED REAGENTS
; FILE REFERENCE: DX0613B
; CURRENT APPLICATION NUMBER: US/10/652,893
; CURRENT FILING DATE: 2003-08-29


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Db      3635 CTACCCAGTGGCGAGTGGAGTACATCACAGGCTCTGGAGTGCACACCTACAAAGCTGTG 3694
QY      180 LeuAlaAsnGlyValLeuSerArg-----AspGlySerLeuSerAspLysArgPheLeu 197
Db      3695 ATTCACTACAGCTGTGAAGACCTTCTACACATGAAGTGAATGATGGTAAATATGTG 3754
QY      198 PheThrSerAsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAla 217
Db      3755 TGTGAGGCTGTAGTATCTCGACGAGCTCCAAAGGAGAAATCACTCCAGTCTCTGTGAG 3814
QY      218 SerSerSerTrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGln 237
Db      3815 CCTGTTTGTGCACTATCAGCCGCCACCAACAGGAGCGGTATATA-TGG----- 3861
QY      238 AlaArgLeuGlnAspGlnGlyProSerTrp-----AlaSerGlyAspSerSer 253
Db      3862 -----AGGCCAAAGGCAAAACCTGTGTGATTTCTTGGCAAGTCTGTATATTAGG 3912
QY      254 AsnAsnHisLysProArg 259
Db      3913 TGGAAACACACAGCAGCAGG 3930

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RESULT 15

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US-11-128-061-787
; Sequence 787, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; PRIOR FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 787
; LENGTH: 2521
; TYPE: DNA
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (642)..(676)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1092)..(1113)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-787

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Alignment Scores:
Fred. No.: 1.28e-07 Length: 2521
Score: 169.00 Matches: 54
Percent Similarity: 49.40% Conservative: 28
Best Local Similarity: 32.53% Mismatches: 60
Query Match: 6.61% Indels: 25
DB: 7 Gaps: 8

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US-10-813-588-2 (1-487) x US-11-128-061-787 (1-2521)

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QY      211 ProAspGlyGlnIleArgAlaSerSerTrpGlnSerValAsnGluSerGlyAspGln 230
Db      109 CCAGATGAGGACATAACAGCTTCAAGTCAGTGGTGCAGA-ATCCAC-----GGCTGCCAG 161

```

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QY      231 ValHisTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSerTrpAla----- 248
Db      162 ATA-----TGGAGGCTGGACTCTGAAGAAGGAGA-----TGGAGCCTGGTG 203
QY      249 SerGlyAspSerSerAsnAsnHisLysPro-ArgGluTrpLeuGluIleAspLeuGlyG1 268
Db      204 TCCGAGATTCCAGTGCACACCCGATGACCTGAAAGAAATTTCTGCAGATTGACTTACGTAC 263
QY      268 uLysLysLysIleThrGlyIleArgThrThrGlySerThrGlnSerAsnPheAsnPhe-- 287
Db      264 CCTCCACTTTTATCACTCTTGTGGGAGCCCGAGGACGTCATGCGGGGGTTCATGGCATTGA 323
QY      288 -TyrValLysSerPheValMetAsnPhelysAsnAsnSerLysTrpLysThrTrpLys 307
Db      324 ATATGCACCCATGTATCAAGATCAACTATAGTCGAGATGGCACTCGCTGGATCTCCTGGGG 383
QY      307 sGlyIleValAsnAsnGluGluLysValPheGlnGlyAsnSerAsnPheArgAspProVa 327
Db      384 TAAT-----CGCATGGAAACAGCGTGTAGATGGAAACAGTAACCTTATGATGCTTT 437
QY      327 lGlnAsnAsnPheIleProIleValAlaArgTyrValArgValValProGlnThrTr 347
Db      438 CCTGAAGGACCTGGAGCCACCCATTGTAGCCAGATTGTTCGCTTATCCAGTCACTGA 497
QY      347 PHis---GlnArgIleAlaLeuLysValGluLeuIleGlyCysGlnIleThrGlnGlyAs 366
Db      498 CCACCTCCATGAATGTGTGCATGAGGGTTGAGCTTTATGTTGT----- 540
QY      366 nAspSerLeuValTrp 371
Db      541 -----GTCTGG 546

```

Search completed: January 15, 2006, 23:30:12
Job time : 412 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2006, 19:27:38 ; Search time 4505 Seconds

(without alignments)

5057.782 Million cell updates/sec

Title: US-10-813-588-2

Perfect score: 2557

Sequence: 1 MTSKNYPGTYPNHTVCEKTI.....YDNEKEMTQKLDITSDMAG 487

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-O=/cpn2.1/USPTO.spool_p/US10813588/runat_12012006_171131_15401/app.query.fasta_1.647
-DB=EST-QPWT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10813588 @CGN 1.1 8010 @runat_12012006_171131_15401 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hgc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

CR749448 3600 bp mRNA linear HTC 19-AUG-2004
LOCUS Homo sapiens mRNA; cDNA DKFZp86L21135 (from clone DKFZp86L21135).
DEFINITION CR749448
ACCESSION CR749448
VERSION CR749448.1 GI:51476605
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 3600)
AUTHORS Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

CONSRWT
TITLE Direct Submission
JOURNAL Submitted (17-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2036	79.6	3600	4 CR749448	
2	1512.5	59.2	1031	3 BM558496	CR749448 Homo sapi
3	1289.5	50.4	839	6 CF785931	BM558496 AGENCOURT
4	1180.5	46.2	961	5 BUI17739	CF785931 AGENCOURT
5	1155.5	45.2	1824	4 AK016485	BUI17739 AGENCOURT
6	1154.5	45.2	2835	4 AK014521	AK016485 Mus muscu
7	1154	45.1	652	7 CN404610	AK014521 Mus muscu

CN404610 170005325

FEATURES

8	1014.5	39.7	866	8	DN134443
9	896	35.0	956	5	BY713935
10	879.5	34.4	913	6	CD109068
11	861	33.7	865	8	CX498307
12	850	33.2	770	6	CB988462
13	820	32.1	864	8	DR845229
14	802	31.4	830	7	CN440576
15	795.5	31.1	872	2	BG245910
16	769	30.1	736	8	CX755002
17	765	29.9	683	5	BX360287
18	762	29.8	805	8	CX417452
19	756	29.6	686	5	BX345014
20	756	29.6	745	5	BU449584
21	747.5	29.2	883	2	BG975603
22	729.5	28.5	935	6	CA986706
23	727	28.4	466	1	AW390343
24	721	28.2	798	6	CB960471
25	707.5	27.7	4121	4	AK051889
26	695.5	27.2	860	3	BJ728454
27	673	26.3	478	10	CG521977
28	661	25.9	434	1	AW483656
29	650	25.4	425	10	C2293584
30	646	25.3	1150	3	BM805721
31	643	25.1	790	6	CB959630
32	642.5	25.1	899	6	CA791785
33	636.5	24.9	802	6	CD110061
34	625	24.4	404	11	DQ039380
35	625	24.4	404	11	DQ039381
36	625	24.4	409	10	C2293317
37	625	24.4	600	5	BU924048
38	624	24.4	462	10	CL639277
39	623	24.4	417	10	C2293527
40	619	24.2	426	10	C2293590
41	614	24.0	402	10	C2293313
42	609	23.8	348	7	CN404612
43	585	22.9	911	8	DN063593
44	582	22.8	857	8	CX889725
45	581.5	22.7	793	7	CK462259

ALIGNMENTS

CR749448 3600 bp mRNA linear HTC 19-AUG-2004
LOCUS Homo sapiens mRNA; cDNA DKFZp86L21135 (from clone DKFZp86L21135).
DEFINITION CR749448
ACCESSION CR749448
VERSION CR749448.1 GI:51476605
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 3600)
AUTHORS Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.

CONSRWT
TITLE Direct Submission
JOURNAL Submitted (17-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY

COMMENT
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project. This clone (DKFZp86L21135) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp86L21135
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES
Location/Qualifiers

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/mol_type="mRNA"
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/clone="DKFZp686L21135"
/tissue_type="prostate"
/clone_lib="686 (synonym: hlcc3). Vector pSport1_sfi; host
DH10B; sites SfiIA + SfiIB"
/dev_stage="adult"
/note="hypothetical protein, N-terminus truncated, not
fully spliced"
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1. .3600
/gene="DKFZp686L21135"
<208. .>606
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ORIGIN
Alignment Scores:
Pred. No.:      2,08e-210      Length:      3600
Score:          2036.00      Matches:      461
Percent Similarity: 43.61%      Conservative: 0
Best Local Similarity: 43.61%      Mismatches: 2
Query Match:      79.62%      Indels:      596
DB:                4          Gaps:        3

US-10-813-588-2 (1-487) x CR749448 (1-3600)

Qy      1 MetThrSerIysAsnTyrProGlyThrTyrProAsnHisThrValCysGluIysThrIle 20
Db      253 ATGACATCTAAGAAATTATCCCGGAGCTACCCCAATCACACTGTTTGCAGAAAGACAAAT 312

Qy      21 ThrValProIysGlyIysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
Db      313 ACAGTACCAAGGGGAAGACTGATCTGAGGTGGGAGATTGGATATCGAATCCAG 372

Qy      41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
Db      373 ACCTGTGCTCTCACTACTCTCTTCCACAGCTCTTCAGATCAATATGTTCCATCTGT 432

Qy      61 GlySerMetThrValProIysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
Db      433 GGAAGTATGACTGTCTCCAAAGAACTCTTGTGAACAAAGTGAAGTAACCGTCCGCTTT 492

Qy      81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
Db      493 GAGAGTGGATCCACATTTCTGCGCGGGTTTTTGTGACCTATGCGAGCAGGACCAT 552

Qy      101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuIysThrGluTyrSerIys 120
Db      553 CCAGATTATAACATGTTTTGGAACGAGCTAGCCATTAATTTGAAGACAGAATACAG --- 608

Qy      121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
Db      608 ----- 608

Qy      141 TyrArgAspThrSerLeuLeuCysIysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
Db      609 -----ACCTCTTTATTGTGAAGCTGCCATCCATGCGAGGAATAATTGCTGATGA 659

Qy      161 LeuGlyGlnIleSerValLeuGlnArgIysGlyIleSerArgTyrGluGlyIleLeu 180
Db      660 CTAGGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGGATCAGTCATATGAAGGGATTCTG 719

Qy      181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspIysArgPheLeuPheThrSer 200
Db      720 GCCAATGGTGTCTTTTCAGGGATGGTTCCCTGTTCAGAACAGCGATTCTGTTCCTCC 779

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Qy      201 AenGlyCysSerArgSerIleuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
Db      780 AATGGTTGCAGCAGATCCTTGAAGTTTGAACCTGACGGGCAAAATCAGAGCTTCTTCTCA 839

Qy      221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnIleArgLeu 240
Db      840 TGGCAGTCGGTCAATGAGAGTGGAGCAAGTTCATCGTCTCTCTGGCCAAAGCCGACTT 899

Qy      241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisIysProArgGlu 260
Db      900 CAGGACCAAGGCCCATCATGGCTTCGGCGCAGCAGTAGCAACAACAACACACGAGAG 959

Qy      261 TrpLeuGluIleAspLeuGlyGlyIysIysIleThrGlyIle----- 275
Db      960 TGGCTGGAGATCGATTTGGGGGAGAAAAAAGAAAAATAACAGGTGC-AGAAAAATAACACAAG 1018

Qy      275 ----- 275

Db      1019 TGCCAAGTGCAGAGTAGTTTCATGACTGTGTAATGACTCGCAGTTGAAAAATACGCTTATT 1078

Qy      275 ----- 275

Db      1079 GTTTACATAGTGCTTCTCTACCTCCCAAGTTCTTGAATATTTTGAABATGTAACAA 1138

Qy      275 ----- 275

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Qy      275 ----- 275

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Qy      275 ----- 275

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Qy      276 -----ArgThrThrGlySer 280
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Db      1439 ACACAGTCGAACTTCAACTTTTATGTTAAGAGTTTTTGTGATGAACCTTCAAAAAACAATAAT 1498

Qy      301 SerIysTrpIysThrTyrIysGlyIleValAsnAsnGluGluIys----- 315
Db      1499 TCTAAGTGAAGACCTTATAAGGAATTTGTGAATTAATGAAGAAAAAGGTAAGAGTAACCCCT 1558

Qy      315 ----- 315

Db      1559 AGAGGCAAGAGGACTGAGTAGGAGAACAGCGCTCTATATATATTTTCATCATGTGTTTACA 1618

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Qy      315 ----- 315

Db      1679 CCAAGCTTTGGGAAGCCAAAGCGAGGAGGATCATTTTGAGACCATCTCTGGGCAACATAGCAA 1738

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Qy      315 ----- 315

Db      1799 TCCTAGATACTTGAAGGCTGAGGCGAGGAAGATCACTTGTGAGCCAGGAGTTCAAGGTTAC 1858

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QY 315 ----- 315
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QY 315 ----- 315
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QY 315 ----- 315
Db 2039 AGCCTGGCCAACATAGTGAACCCCATCTCTACTAAAAATACAAAAATTAGCCAGCGTG 2098
QY 315 ----- 315
Db 2099 GTGGCTGGTCCCTATAATCCAGCTACTTTGGGAGGCTGAGCAGGAGAAATCATTTGAACC 2158
QY 315 ----- 315
Db 2159 TGGGAGCGGAGGTTGTAGTGAGCCGAGATTGACCATTTGCATCTCAGCCTGGGCGACAA 2218
QY 315 ----- 315
Db 2219 GAGCGAGATTCCATCTCAAAAAAAGAAAAAGAAAAAGAAAGATGGGGCTTTCTTGGC 2278
QY 315 ----- 315
Db 2279 ATCCAAATCCAAGAAATAGAAATGTGTCAATAAAACCTTGAGAGATCTTTGTGATTTAA 2338
QY 315 ----- 315
Db 2339 TTCTTTTCTACTTCAGGAATGAATACTTGTGATTTCTTGGGAAGTGAATTTGGCCAT 2398
QY 315 ----- 315
Db 2399 TTAAAAATGCTGCTTCAGTATAAGTATGATGATGTTTGTGAGTTGGACATTTGTCTTGGGA 2458
QY 315 ----- 315
Db 2459 TCCTGTAGTGAATAGAAATTCGGAAGGAATGCAAAAGTGAAGAGCTGAAGCCTT 2518
QY 315 ----- 315
Db 2519 GTGCTCTGAGGTTGCTTCTATAGCACCAGTTGAACTAGGAATATTAAGGTCAATA 2578
QY 315 ----- 315
Db 2579 ATACAACAGGCAATTTTAGCTTCTTTATCCAAATGAATTTAAATCAGTAAACAGTTG 2638
QY 315 ----- 315
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QY 315 ----- 315
Db 2699 TCAAGAGTGTCTAGAAAAATGCAACCGACATAGAATCTTGGCTTGGTTTCATATAACCA 2758
QY 315 ----- 315
Db 2759 GGTATAAGTGGGATGATAAACACCTAAAACTCACTAATAGAACTTAAGGTAAACATAA 2818
QY 316 ----- ValPheGlnGlyAsnSerAsnPheArgAspProValGlnAsnAsnPh 331
Db 2819 TTTCCTCTCTATAGGTGTTTTCAGGTAACCTCTAACTTTTCGGGACCCAGTGCACAAATTT 2878
QY 331 eileProProlleValAlaArgTyrValArgValValProGlnThrThrPheGlnArgTl 351
Db 2879 CATCCCTCCCATCGTGGCCAGATATGTGGGGTGTGCCCCAGACATGGCCACAGAGGAT 2938
QY 351 eAlaLeuLysValGluLeuIleGlyCysGlnIleThrGlnGlyAsnAspSerLeuValTr 371
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Db 2939 AGCCTTGAAGGTGGAGCTCATTTGGTTGCCAGATCACACAAGGTAAATGATTCATTGGTGG 2998
QY 371 pArgLysThrSerGlnSerThrSerValSerThrLysLysGluAspGluThrIleThrAr 391
Db 2999 GCGCAAGCAAGTCAAGCACCAGTGTTCACCTAAGAAAGAAGATGAGACAATCAACAG 3058
QY 391 gProlleProSerGluThrSerThrGlyIleAsnIleThrValAlaIleProLe 411
Db 3059 GCCCATCCCTCGGAAGAAACATCCACAGGAATAACATTACACGGTGGCTATTCCATT 3118
QY 411 uValLeuLeuValValPheAlaGlyMetGlyIlePheAlaAalaPheArgLysLy 431
Db 3119 GGTGCTCTCTTGTCTGCTGTTGCTGGAATGGGATCTTTGCAGCCTTTAGAAAGAA 3178
QY 431 sLysLysLysGlySerProTyrGlySerAlaGluAlaGlnLysThrAspCysTrpLysGl 451
Db 3179 GAAGAAGAAGAAAGATCGGTATGGATCAGCAGAGCTCAGAAACAGACTGTTGGAAGCA 3238
QY 451 nIleLysTyrProPheAlaArgHisGlnSerAlaGluPheThrIleSerTyrAspAsnGl 471
Db 3239 GATTAAATATCCCTTGGCAGACATCAGTCAGCTAGTTTACATCAGCTATGATATGA 3298
QY 471 uLysGluMetThrGlnLysLeuAspLeuIleThrSerAspMetAlaGly 487
Db 3299 GAAGGAGATGACAAAAAGTTAGATCTCATCAAGTGATATGGCAGGT 3347

RESULT 2
BM558496
LOCUS
DEFINITION
5', mRNA sequence.
ACCESSION BM558496
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 1031)
NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12757 row: k column: 11
High quality sequence stop: 694.

FEATURES
Location/Qualifiers
1..1031
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5741314"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_88"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 5,01e-154 Length: 1031
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127 ArgAspValAlaGlyAspIleSerGlyAsnMetValAspGlyTyrArgAspThrSerLeu 146
 Db AGAGAGCTAGCAGACAGACATTTCTGGGAATATGTTAGATGATATAGATACCTCTTTA 67

147 LeuCysGlyValAlaAlaHisAlaGlyIleIleAlaAspGluLeuGlyGlnIleSer 166
 Db TTGTGCAAGCTGCCATCCATGATGAGGAATAATTTGCTGATGAATAGTGGCCAGATCAGT 127

167 ValLeuGlnArgLysGlyIleSerArgTyrGlyGlyIleLeuAlaAsnGlyValLeuSer 186
 Db GTGCTTCAGCGCAAGAGGATCAGTCATATGAGGGATTTCTGCCAATGGTGTCTTTTCG 187

187 ArgAspGlySerLeuSerAspLysArgPheLeuPheThrSerAsnGlyCysSerArgSer 206
 Db AGGGATGGTTCCCTGTGACAGACGATTTCTGTTTACCTCCCAATGTTGCAGCAGATCC 247

207 LeuSerPheGluProAspGlyGlnIleArgAlaSerSerSerTrpGlnSerValAsnGlu 226
 Db TTGAGTGTGTTGAACCTGACGGGCAATCAGAGCTTCTTCTCATGGCAGTCGGTCAATGAG 307

227 SerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyProSer 246
 Db AGTGAGAGCAAGTTCACTGCTCTCTGGCCAGCCCGACTTCAGAGCCCAAGCCCATCA 367

247 TrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGluTrpLeuGluIleAspLeu 266
 Db TGGGCTTCGGGCGACAGTAGCAACACCAACACACGAGAGTGGCTGGAGATCGATTG 427

267 GlyGluLysValLysIleThrGlyIleArgThrThrGlySerThrGlnSerAsnPheAsn 286
 Db GGGGAGAAAAAGAAAAATAACAGGAATTAGGACCAAGGATCTACAGATCGAACTTCAAC 487

287 PheTyrValLysSerPheValMetAsnPheLysAsnAsnAsnSerLysTrpLysThrTyr 306
 Db TTTATGTATGAGGTTTGTGATGAACCTTCAAAAACAATAATTTCTAAGTGGAGACCTAT 547

307 LysGlyIleValAsnAsnGluLysValPheGlnGlyAsnSerAsnPheArgAspPro 326
 Db AAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGGTAACTCTAACTTTCGGGACCCA 607

327 ValGlnAsnAsnPheIleProPheValAlaAlaArgTyrValArgValValProGlnThr 346
 Db GTGCAAAAACAATTTCACTCCCTCCCATCGTGGCCAGATATGTGGGGTGTCTCCCCAGACA 667

347 TrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCysGlnIleThrGlnGlyAsn 366
 Db TGGCACCAGAGATAGCTTTGAAGTGGAGCTCATTTGGTTCAGATTACAAAGTTAT 727

367 AspSerLeuValTrpArgLysThrSerGlnSerThrSerValSerThrLysLysGluAsp 386
 Db GATTCATTGTTGGGCTGCAGAACAGTCAACACCACTTGTTCACCTAGAAATAGAAGAAC 787

387 GluThrIleThrArgProIleProSerGluGlu 397
 Db -----ATCACAGGCCCT---CCCTCTCGAGAA 811

RESULT 4
 BUI77739
 LOCUS BUI77739 961 bp mRNA linear EST 04-SEP-2002
 DEFINITION AGENCOURT_7961999 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:6106770
 5', mRNA sequence.
 ACCESSION BUI77739
 VERSION BUI77739.1 GI:22691723
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 1 (bases 1 to 961)
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2348 row: f column: 19
 High quality sequence stop: 591.

FEATURES

source

1..961
 Location/Qualifiers
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 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_39"
 /note="Organ: pancreas; Vector: pOT87; Site:1: XhoI;
 Site:2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed
 by Ling Hong in the laboratory of Gerald M. Rubin
 (University of California, Berkeley) using ZAP-cDNA
 synthesis kit (Stratagene) and Superscript II RT (Life
 Technologies)."

ORIGIN

Alignment Scores:

Pred. No.: 9,02e-118 Length: 961
 Score: 1180.50 Matches: 236
 Percent Similarity: 90.77% Conservatives: 10
 Best Local Similarity: 87.08% Mismatches: 14
 Query Match: 46.17% Indels: 11
 DB: 5 Gaps: 3

US-10-813-588-2 (1-487) x BUI77739 (1-961)

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 Db 3 TCTTTGAGTGTGTAACCTGACGGGCAAAATCAGAGCTTCTTCTCATGGCAGTCGGTCAAT 62

QY 226 GluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeuGlnAspGlnGlyPro 245
 Db 63 GAGAGTGGAGACCAAGTTCACCTGGTCTCTCTGCCAAGCCCGACTTCAGAGCCAAAGGCCCA 122

QY 246 SerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGluTrpLeuGluIleAsp 265
 Db 123 TCATGGGCTTCGGGCGACAGTAGCAACCAACCAACCAACAGAGTGGCTGGAGATCGAT 182

QY 266 LeuGlyGluLysLysIleThrGlyIleArgThrThrGlySerThrGlnSerAsnPhe 285
 Db 183 TTGGGGGAGAAAAAGAAAAATAACAGGAATTAGGACCAAGGATCTACAGATCGAACTTC 242

QY 286 AsnPheTyrValLysSerPheValMetAsnPheLysAsnAsnAsnSerLysTrpLysThr 305
 Db 243 AACTTTTATGTTAAGAGTGTGTGATGAACCTTCAAAAACAATAATTTCTAAGTGGAGAGCC 302

QY 306 TyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsnSerAsnPheArgAsp 325
 Db 303 TATAAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGGTAACTCTAACTTTCGGGAC 362

QY 326 ProValGlnAsnAsnPheIleProPheValAlaAlaArgTyrValArgValValProGln 345
 Db 363 CCAGTGCAGAAAAAATTTTCATCTCCCTCCCATCGTGGCCAGATATGTGGGGTGTGCCCCAG 422

QY 346 ThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCysGlnIleThrGlnGly 365
 Db 423 ACATGGCACCAGAGATAGCTTTGAAGTGGAGCTCATTTGGTTCAGATTACAAAGT 482

QY 366 AsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerValSerThrLysLysGlu 385


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QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPhelLysAsnAsn 300
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QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
Db 667 -----
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
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Db 668 -----ACACCCCA 676
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValLeuValPheAla 420
Db 677 GGAATGAATATTACAACTGTGGGATTCATCAGTGATCTTCATCGCCCTCTCTGACT 736
QY 421 GlyMetGlyIlePheAlaPheArgLysLysLysLysLysLysGlySerProTyrGlySer 440
Db 737 GGAATGGGGATCTTTGCAATCTGTAGAAAGAGGAAAAAGAAAGAAATCCATATGTGTCA 796
QY 441 AlaGluAlaGlnLysThrAspCysTyrLysGlnIleLysTyrProPheAlaArgHisGln 460
Db 797 GCTGAGCTCAGAAACAGGCTGTGGAAAGCAGATTAATATCCCTTTGCCAGGCATCAG 856
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
Db 857 TCGACCGAATTTACCATCAGCTATGACATGAAAGAGAGATGACACAAAGTTGGATCTC 916
QY 481 IleThrSerAspMetAla 486
Db 917 ATCACTAGTATATGGCA 934

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RESULT 7
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LOCUS 1700532579818 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN404610
ACCESSION CN404610.1 GI:47392155
VERSION EST.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

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REFERENCE 1 (bases 1 to 652)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,X., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 652 Std Error: 0.00.
Location/Qualifiers

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FEATURES

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RESULT 8
DN134443
LOCUS DN134443
DEFINITION 999656 MARC 4P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION DN134443
VERSION DN134443.1 GI:59828760

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source

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/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
/note="Oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

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ORIGIN

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Alignment Scores:
Pred. No.: 3 85e-115 Length: 652
Score: 1154.00 Matches: 217
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.13% Indels: 0
DB: 7 Gaps: 0
US-10-813-588-2 (1-487) x CN404610 (1-652)
QY 120 LysPheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAsp 139
Db 1 AAATTCGCCAGCTGGTTGTAGACAGCTAGCAGGAGACATTTCTGGGAATATGGTAGAT 60
QY 140 GlyTyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleAlaAsp 159
Db 61 GGATATAGAGATACCTCTTTATTGTGCAAGCTGCCATCCATGCGAGGAATAATTGCTGAT 120
QY 160 GluLeuGlyGlyGlnIleSerValLeuGlnArgLysGlyLysArgTyrGluGlyIle 179
Db 121 GAACTAGGTGGCCAGATCAGTGTGTTTCAGCCCAAGGGATCAGTCGATATGAGGGATT 180
QY 180 LeuAlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThr 199
Db 181 CTGGCCAAATGGTGTCTTTCGAGGGATGTTCCCTGTGACAGCAAGGATTTCTGTTTACC 240
QY 200 SerAsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSer 219
Db 241 TCCAAATGGTTGCAGCAGATCCTTTGAGTTTGAACCTGACGGGCAATCAGAGCTTCTTCC 300
QY 220 SerTrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArg 239
Db 301 TCATGGCAGTCCGTCATGAGAGTGGAGCCAGTTCTACTGTCTCTCTGCGCCACGCCGA 360
QY 240 LeuGlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArg 259
Db 361 CTTCAGGACCAAGGCCCATCATGGCTTCGGGCGACAGTAGCAACAACCAACCAACCA 420
QY 260 GluTrpLeuGluIleAspLeuGlyGlyLysLysIleThrGlyIleArgThrThrGly 279
Db 421 GAGTGGCTGGAGATCGATTTGGGGAGAAAAAGAAATAACAGGAATTAGGACCAACAGA 480
QY 280 SerThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPhelLysAsn 299
Db 481 TCTACACAGTCGACTTCACTTTTATGTTAGAGTTTGTGATGATCACTTCAAAACAAT 540
QY 300 AsnSerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGly 319
Db 541 AATTCTAAGTGAAGACCTATAAAGAAATTTGGAATAATGAAGAAAGGTGTTTCAGGT 600
QY 320 AsnSerAsnPheArgAspProValGlnAsnAsnPheIleProProIleVal 336
Db 601 AACTTAACTTTTCGGGACCCAGTGCAGAAACAATTTTCATCCCTCCCATCGT 651

```


Email: genome-res@gs.riken.jp, URL: <http://genome.gsc.riken.jp/>
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
 Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
 Imokani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
 Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
 Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
 Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
 Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.

FEATURES

Location/Qualifiers
 1..956
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="4631413K11"
 /sex="mixed"
 /tissue_type="skin"
 /dev_stage="0 day neonate"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, 0 day neonate
 skin"

/note="Site_1: SalI; Site_2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 10.0 and subtraction to Rot = 100.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5' GAGAGAGATTCGAGTTAATTAATTCCTCCCTCCCTCC
 3']. cDNA was cloned into the XhoI and BamHI sites.
 Vector: a modified pBluescript KS(+) after bulk excision
 from Lambda FLC I"

ORIGIN

Alignment Scores:

Pred. No.:	1.15e-86	Length:	956
Score:	896.00	Matches:	202
Percent Similarity:	47.95%	Conservative:	32
Best Local Similarity:	41.39%	Mismatches:	52
Query Match:	35.04%	Indels:	203
DB:	5	Gaps:	2

US-10-813-588-2 (1-487) x BY713935 (1-956)

Qy	1	MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle	20
Db	69	ATGACATCTAAGATTATCCAGGGGACTTACCCCAATTACACTGTGTGTGAAGATCATC	128

Qy	21	ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyValAspLeuAspIleGluSerGln	40
Db	129	ACAGTCCCAAGGGGAGAGACTTATCTGAGTTGGGAGATTGAGCAATTGAGTCCAAG	188
Qy	41	ThrCysAlaSerAspTyrIleLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys	60
Db	189	ACCTGCGCTTCTGACTATCTCTCTTCAGCAGTGCAACAGATCAGTATGTTCCATATTGT	248
Qy	61	GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe	80
Db	249	GGGAGTTGGCTGTTCCTCCCAAGAACTCCGGCTGAACTCAACAGAAAGTGAATGCTCTTC	308
Qy	81	GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis	100
Db	309	AAGAGTGGATCTCACATTTCTGCGCGGGCTTCTGCTGACCTACGCCAGCAGTGCACAT	368
Qy	101	ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys	120
Db	369	CCAGATTTTAATAACCTGTTTGGACGAGGAGCCCATTTATTCGAGGAAAAATACAGCAAA	428
Qy	121	PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerClyAsnMetValAspGly	140
Db	429	TTCTCCCGCAGCTGGCTGTAGACATAGCAGAGATATTTCTGGGAATACAAAAGATGTT	488
Qy	141	TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu	160
Db	489	TACAGAGATACCTCTTTATTTGTCGAAGCTGCCATCCAGCGGGATCATCAGATGAA	548
Qy	161	LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu	180
Db	549	CTAGTGGGCCACATCAACTTGCTTCAGACGAAGGGATAAGTCACTATAGAGGACTCCTG	608
Qy	181	AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer	200
Db	609	GTCAATGGCGTCTCTCCGCGCATGTTCTTTGTGGAAGAGCGATTTCTTTT	662
Qy	201	AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer	220
Db	662	-----	662
Qy	221	TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu	240
Db	662	-----	662
Qy	241	GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerSerAsnAsnHisLysProArgGlu	260
Db	662	-----	662
Qy	261	TrpLeuGluIleAspLeuGlyGlyLysLysIleThrGlyIleArgThrThrGlySer	280
Db	662	-----	662
Qy	281	ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn	300
Db	662	-----	662
Qy	301	SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn	320
Db	662	-----	662
Qy	321	SerAsnPheArgAspProValGlnAsnAsnAsnPheIleProProIleValAlaArgTyrVal	340
Db	662	-----	662
Qy	341	ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys	360
Db	662	-----	662
Qy	361	GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal	380
Db	662	-----	662
Qy	381	SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr	400

Tel: 925 296 5600
 Fax: 925 296 5710
 Email: cdna@jgi-psf.org
 Tissue Procurement: Richard M. Harland Laboratory, University of California, Berkeley: <http://tropicalis.berkeley.edu/home>
 cDNA Library Preparation: Richard M. Harland Laboratory, University of California, Berkeley
 DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>
 Clone Distribution: I.M.A.G.E. Consortium/LLNL:
<http://image.llnl.gov>
 Naming Conventions: EST name is generated by the concatenation of the JGI Clone id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
 Plate: XZG 0457 row: a column: 20
 High quality sequence stop: 802.

FEATURES

Location/Qualifiers
 1..865
 /organism="Xenopus tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="IMAGE:7558558"
 /tissue_type="whole embryo"
 /dev_stage="Gastrula (st. 10.5-12.5)"
 /lab_host="E. coli XL1-Blue derivative, Stratagene ElectroTen-Blue"
 /clone_lib="NIH XGC tropGas7"
 /note="Vector: pCSI08; Site 1: SalI; Site 2: NotI; Gastrula library constructed by Russell B. Fletcher in R. Harland's lab using poly A RNA and oligo dT primers (Invitrogen SuperScript Plasmid System for cDNA Synthesis and Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted into vector pCSI08
 (http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)"

ORIGIN

Alignment Scores:
 Pred. No.: 6,61e-83 Length: 865
 Score: 861.00 Matches: 167
 Percent Similarity: 74.65% Conservative: 48
 Best Local Similarity: 57.99% Mismatches: 63
 Query Match: 33.67% Indels: 10
 DB: 8 Gaps: 4

US-10-813-588-2 (1-487) x CX498307 (1-865)

QY 120 LysPheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAsp 139
 :::
 Db 3 AGGTTCTGTCGGCTGGTTCGAAAGATGTAGCTGGGATATCTCAGGAGATGTGGTGGAA 62
 QY 140 GlyTyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAsp 159
 :::
 Db 63 GGATACAGAGATACCTCTCTGCTTTGCAAGCTGCGATTCATGCTGGATTTATTCAGAT 122
 QY 160 GluLeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIle 179
 :::
 Db 123 GAACCTGGGGGACAGATTACGTGTACACGACACAAAGGTATACCGCATACAGAGCTTT 182
 QY 180 LeuAlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThr 199
 :::
 Db 183 CTGGCCACCGCATCTTGTCAAAAGATGGTCACTTTCAGACCATCGGTTGTGTAGTA 242
 QY 200 SerAsnGlyCysSerArgSerLeuSer-----PheGluProAspGlyGlnIleArgAla 217
 :::
 Db 243 GGTCTGTACTGACGCTTATCTCTGTACGTGGGGTTTGAAAAGAT---AAGTTTTCAGCC 299
 QY 218 SerSerSerTyrGlnSerValAsnGluSerGlyAspGlnValHisTyrSerProGlyGln 237
 :::
 Db 300 ACCTGCTTATCACTGGACAGTGAACAGGGGAGATTAAAGTCTGTGTGCTGTAAGA 359
 QY 238 AlaArgLeuGlnAspGlnGlyProSerTyrAlaSerGlyAspSerSerAsnAsnHisLys 257
 :::

Db 360 GCACAGCTTAAACACACACAGGCATTTCTGGGCTTCTGTATCACCAGTCCAGT----- 410
 QY 258 ProArgGluTyrLeuGluIleAspLeuGlyGluLysLysIleThrGlyIleArgThr 277
 Db 411 ---CGGAATGGTTAGAAATCGACCTAGGGGAAAAAATAAATAATGATTTGTGACC 467
 QY 278 ThrGlySerThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLys 297
 Db 468 GCAGGATCCACATCACAAAATTTAACTTTTATGTAATCTTATATCATCACTTTAGA 527
 QY 298 AsnAsnAsnSerLysTyrLysThrTyrLysGlyIleValAsnAsnGluLysValPhe 317
 Db 528 CGGGATGGATCAAAATGGAAGCTTTATAAGGGAGCTGTGAGCAATCAGGAAAGAGATTG 587
 QY 318 GlnGlyAsnSerAsnPheArgAspProValGlnAsnAsnPheIleProIleValAla 337
 Db 588 GAAGGCAACTTAAATTTATATGACAGGGCAGCAACAATTTTATCTCTATAGTGGCT 647
 QY 338 ArgTyrValArgValValProGlnThrTyrHisGlnArgIleAlaLeuLysValGluLeu 357
 Db 648 CGGTATCTGAGAAATCACACCCCAACCTCGAATGAAGAATTGCTTTGAAGGTGAGCTT 707
 QY 358 IleGlyCysGlnIleThrGlnGlyAsnAspSerLeu-----ValTyrArgLysThr 374
 Db 708 ATGGGATGCCATTTAGCACAGACACACAATTCATCCACTCATCTATGTGGAAGAAGACA 767
 QY 375 SerGlnSerThrSerValSerThrLysLysGluAspGluThrIleThrArgProIlePro 394
 Db 768 AATGATCTTAGCAAGAACACCGCTTACTAGGAAGAAAGCCATCAGGAGTTGTTCCT 827
 QY 395 SerGluGluThrSerThrGlyIle 402
 Db 828 GCTGAAGATCAAAATCTGGGGATG 851

RESULT 12
 CB988462
 LOCUS
 DEFINITION CB988462 770 bp mRNA linear EST 01-MAY-2003
 IMAGE:30342255 5', mRNA sequence.
 CB988462
 VERSION CB988462.1 GI:30282982
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 770)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDAM375 row: a column: 16
 High quality sequence stop: 607.
 Location/Qualifiers
 1..770
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 /clone="IMAGE:30342255"
 /tissue_type="Human Placenta"
 /lab_host="DH10B Tona"
 /clone_lib="NIH MGC_147"
 /note="Organ: placenta; Vector: pBluescriptR; Site_1:"

all-XhoI; Site 2: BamH; Oligo-dT primed using primer 5'-TTTTTTTTTTTTT-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: This is a NIH_MGC library."

ORIGIN

Alignment Scores:
Pred. No.: 8,76e-82 Length: 770
Score: 850.00 Matches: 166
Percent Similarity: 98.22% Conservative: 0
Best Local Similarity: 98.22% Mismatches: 1
Query Match: 33.24% Indels: 2
DB: 6 Gaps: 0

US-10-813-588-2 (1-487) x CB988462 (1-770)

QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB 268 ATGACATCTAAGAAATTATCCGGGAGCTACCCCAATCACACTGTTTGGAAAGACAATT 327
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuSerGln 40
DB 328 ACAGTACCAAGGGGAAAGACTGATCTGAGGTGGGAGATTGGATATCGAATCCCGAG 387
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
DB 388 ACCTGTGCTCTGACTATCTCTCTCCACAGCTCTTCAGATCAATATGTCATCTGTT 447
QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
DB 448 GGAAGTATGACTGTTCCCAAGAACTCTGTTGACACAGTGAAGTAAACCGTCGGCTTT 507
QY 81 GluSerGlySerHisLeuSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 508 GAGAGTGGATCCACATCTTCTGGCCGGGTTTCTGTCACCTATGCGAGCAGCACCAT 567
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
DB 568 CCAGATTATAACATGTTTGGACGAGCTAGCCATTTATTTGAAGACAGAAATACGCAA 627
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspG1 140
DB 628 TTCTGCCAGCTGGTTGATAGAGCTGACGAGGAGACATTTCTGGGAATATGTTAGATGG 687
QY 140 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleAlaAspG 160
DB 688 ATATAGATACCTCTTTATTTGTGCAAGCTGCCATCCATGCAAGGAATAATTGCTGATG 747
QY 160 IuLeuGlyGlyGlnIleSerVal 167
DB 748 AACTAGTGGCCAGATCATTTGTG 770

RESULT 13

DR845229

LOCUS

DEFINITION JGI_CABE10279.fwd NIH_XGC_tropOval Xenopus tropicalis cDNA clone

IMAGE:7828804 5', mRNA sequence.

ACCESSION

VERSION DR845229.1 GI:71501083

KEYWORDS

SOURCE EST.

ORGANISM

Xenopus tropicalis (western clawed frog)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

REFERENCE 1 (bases 1 to 864)

AUTHORS Richardson,P., Lucas,S., Rokhsar,D., Dettter,J.C., Ng,D.C.,

Brokstein,P. and Lindquist,E.A.

TITLE DOE Joint Genome Institute Xenopus tropicalis EST project

JOURNAL
COMMENT

Unpublished (2004)
Other ESTs: JGI_CABE10279.rev
Contact: Lindquist,E.A., Richardson,P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Robert M. Grainger
cDNA Library Preparation: Bruce Blumberg Laboratory, University of
California, Irvine
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LNLN:
http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone Id and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Plate: CABE 0105 row: n column: 2
High quality sequence stop: 766.

FEATURES

source

1..864
Location/Qualifiers
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/strain="N6 (Nigerian 6th generation inbred)"
/db_xref="taxon:8364"
/clone="IMAGE:7828804"
/sex="Female"
/tissue_type="Ovary"
/dev_stage="Adult"
/lab_host="ElectroMAX DH10B T1 Phage Resistant cells"
/note="Vector: pCSI07; Site 1: EcoRI; Site 2: XhoI; The library was prepared from 5 ug of poly A+ RNA by oligo-dT priming
(5'-ACTAGTCGCGCGCTAGCTCGAGTTTCTTTTCTTTTCTTTT-3') and
Stratascript reverse transcriptase. After ligation of
EcoRI adapters (5'-AATTCGACGAG-3') followed by kinasing
adapters and by XhoI digestion, the cDNA was size selected
by chromatography on Sepharose CL-2B columns and fractions
containing cDNAs larger than 1000 bp were ligated into
EcoRI/XhoI-digested pCSI07. Reference for library
construction: Current Genomics 4, 635-644. Library
constructed by Michelle Tabb and Bruce Blumberg (Dept of
Developmental and Cell Biology, University of California,
Irvine)."

ORIGIN

Alignment Scores:
Pred. No.: 2.01e-78 Length: 864
Score: 820.00 Matches: 163
Percent Similarity: 75.00% Conservative: 38
Best Local Similarity: 60.82% Mismatches: 57
Query Match: 32.07% Indels: 10
DB: 6 Gaps: 6

US-10-813-588-2 (1-487) x DR845229 (1-864)

QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB 74 CTAACATCTAAGAAATTATCCCTGGACATACCCCTAACCAACACTTTGTAAATAACTCTC 133
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuSerGln 40
DB 134 AAAGTACAAACTGGCAAAAGCCTCTATATTATGCTGGCAGATGTAGACATAGAAATCTCGG 193
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyPro 58
DB 194 GATTGTGAATCGGCATATCTGAAAATCTTTAAAGGAACCTTCATCTGAGGAGATAGCTAGC 253
QY 59 TyrCysGlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThr 77
DB 254 TACTGTGGAGATCAGAAACTATACCAAGGAAATGCTCTTGAATACCAATGAAGCCACC 313

QY 78 ValArgPheGluSerGlySerHisIleSerGlyValArgGlyPheLeuLeuThrTyrAlaSer 97
 :::
 Db 314 ATCCACTTTGAGAGTGAATTCATGTCTGGAGTGGATTTTGTCTTAACGCAAGC 373
 QY 98 SerAspHisProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuIleThrGlu 117
 Db 374 AGTGATATCCAGATCTGATACATCGCTGGCAAGATCTAATCATTTATAAGACATAGAA 433
 QY 118 TyrSerLysPheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAenMet 137
 Db 434 TACAGCAGGTTCTGTCCAGCTGTTCCAAAGATGTAGCTGGGATATCTCAGAGATGTG 493
 QY 138 ValAspGlyTyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIle 157
 Db 494 GTGGAAGGATACAGAGATACCTCTGTCTTGCAGAGCTGGCATTCATCTGGAGTTAT 553
 QY 158 AlaAspGluLeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGlu 177
 Db 554 GCAGATGAATCTGGGGGACAGATTCAGGTGAACACGACACAAAGGTATCAGCCGATACAGA 613
 QY 178 GlyIleLeuAlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeu 197
 Db 614 GGCCTTCTGGCAACGCGCATCTGTCCAAAGATGGGTCTCTTCAGACCATCGGGTTGTG 673
 QY 198 PheThrSerAsnGlyCysSerArgSerLeuSer-----PheGluProAspGlyGlnIle 215
 Db 674 TTTAGAGGCTCTGACTGAGCTATCTTGTAGCTGGGGTTTGGAAAAAT---AGTTT 730
 QY 216 ArgAlaSerSerSerTrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerPro 235
 Db 731 TCAGGCACCTCGCTTATCACTGGAACAGTGAACAGGGGAGATTAAAGTCTTGGTGCCT 790
 QY 236 GlyGlnAlaArgLeuGlnAspGlyProSerTrpAlaSerGlyAspSerSerAsnAsn 255
 Db 791 GAAAGAGCAGACCTTAAACACAGAGCATTTCTCGGGCTTCTGATCACCAGTCCAGT--- 847
 QY 256 HisLysProArgGluTrpLeuGlu 263
 Db 848 -----CGGGAATGGTTAGAA 862

RESULT 14

CN440576
 LOCUS BE04022B1F09 BE04 Normalized and Subtracted bovine embryonic and extraembryonic tissue Bos taurus CDNA clone BE04022B1F09 5', mRNA sequence.
 DEFINITION

ACCESSION CN440576.1 GI:46419840

VERSION EST.

KEYWORDS Bos taurus (cow)

SOURCE ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 830)
 AUTHORS Lewin,H.A., Renard,J.P., Yang,X.J., Hernandez,A., Degrelle,S., Hue,I., Tian,X.C., Liu,L. and Everts,R.E.

TITLE Bovine embryonic ESTs
 JOURNAL Unpublished (2004)

COMMENT Contact: Harris Lewin
 Department of Animal Sciences
 University of Illinois at Urbana-Champaign
 206 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL 61801, USA

Tel: 217 333 5998
 Fax: 217 244 5617
 Email: h-lewin@uiuc.edu

Funding for embryonic EST sequencing was provided by USDA ARS Contract No. 58-1275-2-020 to H. A. Lewin. Base Calling/Quality Scores: PHRED 5.2-020 to H. A. Lewin. Base Calling/Quality

Trimming: Cross match from Washington University Genome Center PHRAP suite. Sequences submitted are vector free and at least 200

' bp in length with average PHRED score > 20.

PCR PRIMERs

FORWARD: CCAGTCAGACGCTGTGTAACACAC (M13 NIA-F)

BACKWARD: GTGTGGATTTGTGAGCGGATACAA (M13 NIA-R)

Insert length: 830 Std Error: 0.00

Plate: BE04022B1 row: F column: 09

Seq primer: TTAATACGACTCATATAGGG (T7 PROMOTER)

High quality sequence stop: 830.

FEATURES

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 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone="BE04022B1F09"
 /tissue_type="embryo (day 36 and day 64) and extra-embryonic tissue (day 14 to 25) Normalized and twice subtracted library"
 /lab_host="DH10B"
 /clone_lib="BE04 Normalized and Subtracted bovine embryonic and extraembryonic tissue"
 /note="Vector: pGEMZf1(+); Site 1: EcoRI; Site 2: NotI; The cDNA library was constructed, normalized and subtracted by Dr. A. Hernandez, W.M. Keck Center, University of Illinois Urbana-Champaign and S. Degrelle, BDR, Institut National de la Recherche Agronomique, France, as described in Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996) Genome Research 6(9): 791-806. This clone is from library BE04, a normalized library of embryonic tissues subtracted with 7800 known placental EST sequences and 5000 clones from the BE03 library. The double stranded cDNA was size selected (more than 450 bp), adapted with EcoRI adaptors at both ends and then digested with NotI. The cDNA was then directionally cloned into EcoRI-NotI digested pGEM11zf(+) phagemid vector. Insert size was between 450-2200 bp. Sequencing was done from the 5' end of the clone. Tagged oligo-dT was used to identify the source of the ESTs where possible. (A18)TGGGT = extraembryonic tissue; (A18)TCGGT = 36-day old fetus; (A18)TCGGA = 64-day old fetus (body)"; (A18)TCGGA = 64-day old fetus (body)";

ORIGIN

Alignment Scores:
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 Score: 802.00 Matches: 157
 Percent Similarity: 88.44% Conservative: 19
 Best Local Similarity: 78.89% Mismatches: 18
 Query Match: 31.36% Indels: 6
 DB: 7 Gaps: 2
 US-10-813-588-2 (1-487) x CN440576 (1-830)
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 Db 1 TTTGTAAATGAATTCAGAAACCAACCACTCAAGTGGCAATCTATATAAGGAATTGTGAAT 60
 QY 312 AsnGluGluValPheGlnGlyAsnSerAsnPheArgAspProValGlnAsnAsnPhe 331
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 QY 352 AlaLeuLysValGluLeuIleGlyCysGlnIle-----ThrGlnGlyAsnAsp 367
 Db 181 GCCTTGAAGTGGAGCTCTCTGTTGTCAGGTTGCACCAAGCAGGACGCAAGGTAATGAC 240
 QY 368 SerLeuValTrpArgLysThrSerGlnSerThrSerValSerThrLysLysGluAspGlu 387
 Db 241 TCACGTGGTGGCACA--ACAAGTGTGAATCTGTGGTTCACGAAAGAGAGATAAG 298
 QY 388 ThrIleThrArgProIleProSerGluGluThrSerThrGlyIleAsnIleThrThrVal 407

[illegible]

RESULT 15	872 bp	mRNA	linear	EST 13-FEB-2001
BG245910				
LOCUS				
DEFINITION				
	BG245910	602358725F1	NCI_CGAP_Mam1	Mus musculus cdna clone IMAGE:4486950 5', mRNA sequence.

ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;	
Sciurognathi; Muridae; Murinae; Mus.	

REFERENCE
1 (bases 1 to 872)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

CONTACT: Robert Strausberg, Ph.D.
Email: cgsabbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrived by: The I.M.A.G.E. Consortium
(LLNL)

clone library arrayed by the I.M.A.G.E. Consortium (LNLN).
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>

info: // image name: 9
 plate: LLAM10331 row: b column: 07
 High quality sequence stop: 786.

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FEATURES
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n.9n quarry sequence map: 700.
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/strain="FVB/N"
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/note="Organ: mammary; Vector: pCMV
Site2: NotI; Cloned unidirectional
Library constructed by Life Technol
providing samples: Gilbert Smith, N

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Qy	41	ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys	60
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Qy	61	GlySerMetThrValProLysGluLeuLeuLeuAnthrSerGluValThrValArgPhe	80
Db	368	GGGAGTTGGGCTGTTCCTCAAAGAACTCCGGCTGAACCTCAAACGAAGTGACTGTCTCTTC	427
Qy	81	GluSerGlySerHisIleSerGlyVargGlyPheLeuLeuThrTyrAlaSerSerAspHis	100
Db	428	AAGAGTGGATCTCACATTTCTGGCGGGGCTTTCTGCTGACCTACGCCAGCAGTGCACCAT	487
Qy	101	ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys	120
Db	488	CCGATTTAATAACCTGTTTGGAACGAGCGACCCATTATTTTCGAGGGAAAAATACAGCAAA	547
Qy	121	PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly	140
Db	548	TTCTGCCCCAGCTGGCTGTAGAGACATAGCAGAGATATTTCTGGAGNATACAAAAGATGGT	607
Qy	141	TyrArgAspThrSerLeu-LeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGly	160
Db	608	TACAGATACCTCTTTTATGTGTCAAGCTGCATCCACGCAGGGGGATCATCACAGATGA	667
Qy	160	uLeuGly-GlyGlnIleSerValLeuGlnArgLysGly---IleSerArgTyrGluGlyI	179
Db	668	ACTAGTGGGGCCATCACTATGCTTCAGACCAAGGGGATAAGTFCACCTATTGTAAGGAC	727
Qy	179	IleLeu-AlaGlnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPhe	198
Db	728	TCTTGGGCCAATGGGGTGCTCTCCGGCATGGTCCCTTGTGGAAAGCGATTCITTTTTA	787
Qy	199	ThrSer	200
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Search completed: January 15, 2006, 23:02:58
Job time : 4521 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2006, 17:51:33 ; Search time 726 Seconds
(without alignments)
4470.668 Million cell updates/sec

Title: US-10-813-588-2

Perfect score: 2557

Sequence: 1 MTSKNYPGTPYPHVTCEKTI.....YDNEKEMTKQLDITSDMAG 487

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=N Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10813588 @CGN 1.1.1096 @runat_12012006_171131_15381 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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1: Geneseqn1980s:*
2: Geneseqn1990s:*
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13: Geneseqn2004bs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2557	100.0	1620	4	AAS00615 Novel hum
2	2557	100.0	1761	4	AAS00614 Novel hum
3	2557	100.0	1761	11	Adn39765 Cancer/an
4	2557	100.0	1768	4	AAS00613 Novel hum

5	2557	100.0	2010	11	ADN39764	Cancer/an
6	2557	100.0	2010	13	ADR46610	Cancer-as
7	2557	100.0	2010	13	ADR46611	Cancer-as
8	2551	99.8	2145	8	ACD66718	Secreted
9	2551	99.8	2145	12	ADQ10135	Human pol
10	2551	99.8	2888	6	ADT28055	Adi128055 ECMCAD ge
11	2551	99.8	3151	6	ABN86493	Human neu
12	2551	99.8	3594	4	AAS00660	Human TAN
13	2551	99.8	3594	8	ACD66717	Secreted
14	2551	99.8	3594	12	ADQ10134	Human pol
15	2551	99.8	3676	5	ADL62155	Human ova
16	2512.5	98.3	2547	11	ADM02314	Human cDN
17	2259	88.3	2310	11	ADM39766	Cancer/an
18	2020	79.0	2145	6	ABN86496	Human zcu
19	1322.5	51.7	1265	6	ABN86495	Human cDN
20	1322.5	51.7	1265	6	ABK49565	Human cDN
21	1322.5	51.7	1265	10	ADC29936	Human nov
22	1313.5	51.4	1538	8	ACA10145	Human NOV
23	1313.5	51.4	1538	12	ADO08322	Human NOV
24	1154.5	45.2	2836	6	ABN86494	Mouse zcu
25	1146.5	44.8	1871	3	AAA96736	Polynucle
26	1003	39.2	2473	11	ADM03690	Human cDN
27	1003	39.2	2473	14	ADY18582	DNA encod
28	989	38.7	636	8	ACA10146	Human NOV
29	984	38.5	636	12	ADO08324	Human NOV
30	974	38.1	596	14	ADV74982	Human col
31	920	36.0	2868	6	ABN86495	Mouse zcu
32	881.5	34.5	1509	6	ABN86497	Mouse zcu
33	867.5	33.9	2310	9	ADA00878	Rat ESDN
34	860.5	33.7	2280	8	ABX93042	Human LCC
35	860.5	33.7	2328	9	ADA00874	Human ESD
36	860.5	33.7	5657	8	ABX77581	Different
37	860.5	33.7	5657	10	ADJ56259	Human cDN
38	860.5	33.7	6093	10	ADA19345	Human ins
39	860.5	33.7	6595	12	ADQ23685	Human 8of
40	856.5	33.5	2310	9	ADA00876	Mouse ESD
41	842.5	32.9	2200	6	ABA00056	CADHP-3 c
42	838	32.8	2428	4	AH34855	Human col
43	837.5	32.8	2020	10	ADA53293	Human cod
44	834.5	32.6	6106	13	ACN41353	Human dia
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ALIGNMENTS

RESULT 1

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ID AAS00615 standard; cDNA; 1620 BP.

XX AAS00615;

XX 29-AUG-2001 (first entry)

XX Novel human protein (NHP) DNA sequence #3.

XX Novel human protein; NHP; CUB domain; extracellular domain; gene therapy;
KW obesity; high blood pressure; connective tissue disorder; infertility;
KW NHP-mediated pathway; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1620

FT /*tag= a

FT /product= "Novel human protein #3"

PN WO200129219-A1.

XX 26-APR-2001.

XX 08-OCT-2000; 2000WO-US028798.

XX 19-OCT-1999; 99US-0160285P.

PR 18-FEB-2000; 2000US-0183583P.
XX (LEXI-) LEXICON GENETICS INC.
XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
PI Sands AT;
XX WPI; 2001-290917/30.
DR P-PSDB; AAU00630.
XX Novel nucleic acid encoding human CUB-domain containing protein, useful
PT for drug screening, diagnosis and treatment of physiological disorders or
PT diseases.
XX Disclosure; Page 28-29; 33pp; English.
PS
XX The sequence represents a polynucleotide which encodes a novel human
CC protein (NHP) containing a CUB domain (an extracellular domain). CUB
CC proteins have been associated with regulating development, modulating
CC cellular processes and preventing infectious disease. NHP nucleotide
CC sequences are useful for gene therapy of physiological disorders or
CC diseases. NHP oligonucleotides are useful as hybridisation probes for
CC screening libraries and assessing gene patterns. NHP nucleotide sequences
CC are useful for detecting mutant or inappropriately expressed NHPs (for
CC example, those proteins associated with obesity, high blood pressure,
CC connective tissue disorders and infertility) for the diagnosis of a
CC disease. The polynucleotides may also be used in screening for drugs
CC effective in the treatment of symptomatic or phenotypic manifestations of
CC perturbing the normal function of NHP in the body. Nucleotide constructs
CC encoding NHP products are used to genetically engineer host cells to
CC express such products in vivo. These host cells allow for the
CC identification of compounds that bind to NHP receptors or trigger NHP-
CC mediated pathways
XX
SQ Sequence 1620 BP; 456 A; 353 C; 422 G; 389 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,41e-226 Length: 1620
Score: 2557.00 Matches: 487
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-813-588-2 (1-487) x AAS00615 (1-1620)

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Qy	21	ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln	40
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Qy	61	GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe	80
Db	337	GGAAAGTATGACTGTCTCCCAAGAACTCTTGTGTGAACAACAAGTGAAGTAAACCGTCGCTTT	396
Qy	81	GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis	100
Db	397	GAGAGTCGATCCACATTTCTGGCGGGGTTTTTTTGTGACCTATGAGCAGCGACCAT	456
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Qy	121	PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly	140
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Qy	181	AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer	200
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Qy	221	TyrGlnSerValAsnGluSerGlyAspGlnValHisTyrSerProGlyGlnAlaArgLeu	240
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Db	1477	GCAGAGGCTCAGAAAAACAGACTGTGGAAAGCAGATTAATAATATCCCTTTCGACAGATCAG	1536
Qy	461	SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu	480
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Qy	481	IleThrSerAspMetAlaGly	487
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RESULT 2

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ID AAS00614 standard; cDNA; 1761 BP.

XX AAS00614;

XX 29-AUG-2001 (first entry)

XX Novel human protein (NHP) DNA sequence #2.

XX Novel human protein; NHP; CUB domain; extracellular domain; gene therapy;
KW obesity; high blood pressure; connective tissue disorder; infertility;
KW NHP-mediated pathway; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FT CDS 1..1761

FT /*tag= a

FT /product= "Novel human protein #2"

XX W0200129219-A1.

XX 26-APR-2001.

XX 08-OCT-2000; 2000WO-US028798.

XX 19-OCT-1999; 99US-0160285P.

XX 18-FEB-2000; 2000US-0183583P.

XX (LEXI-) LEXICON GENETICS INC.

XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;

XX Sands AT;

XX WPI; 2001-290917/30.

XX P-PSDB; AAU00629.

XX Novel nucleic acid encoding human CUB-domain containing protein, useful
PT for drug screening, diagnosis and treatment of physiological disorders or
PT diseases.

XX Claim 1; Page 27; 33pp; English.

XX The sequence represents a polynucleotide which encodes a novel human
CC protein (NHP) containing a CUB domain (an extracellular domain). CUB
CC proteins have been associated with regulating development, modulating
CC cellular processes and preventing infectious disease. NHP nucleotide
CC sequences are useful for gene therapy of physiological disorders or
CC diseases. NHP oligonucleotides are useful as hybridisation probes for
CC screening libraries and assessing gene patterns. NHP nucleotide sequences
CC are useful for detecting mutant or inappropriately expressed NHPs (for
CC example, those proteins associated with obesity, high blood pressure,
CC connective tissue disorders and infertility) for the diagnosis of a
CC disease. The polynucleotides may also be used in screening for drugs
CC effective in the treatment of symptomatic or phenotypic manifestations of
CC perturbing the normal function of NHP in the body. Nucleotide constructs
CC encoding NHP products are used to genetically engineer host cells to
CC express such products in vivo. These host cells allow for the
CC identification of compounds that bind to NHP receptors or trigger NHP-
CC mediated pathways

XX Sequence 1761 BP; 471 A; 402 C; 483 G; 405 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4,96e-226 Length: 1761
Score: 2557.00 Matches: 487
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-813-588-2 (1-487) x AAS00614 (1-1761)

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QY	21	ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln	40
DB	358	ACAGTACCAAGGGGAAAGACTGATTCCTGAGGTGGGAGATTGGATATCGAATCCAG	417
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QY	81	GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis	100
DB	538	GAGAGTGGATCCACATTTCTGCCCGGGTGTTCCTGCTGACCTATGCGAGCAGCACCAT	597
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DB	778	CTAGGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATGAAGGGATTCTG	837
QY	181	AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer	200
DB	838	GCCATATGTTGTTCTTTCCAGGGATGTTCCCTGTGACACACAGCATTTCTGTTTACCTCC	897
QY	201	AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer	220
DB	898	AATGTTGCGACAGATCCTTGAGTTTGAACCTGACGGGCAATCAGAGCTTCTTCCTCA	957
QY	221	TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu	240
DB	958	TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTCACTGCTCTCTGCGCCAAAGCCGACTT	1017
QY	241	GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu	260
DB	1018	CAGGACCAAGGCCCATCATGCGCTTCGGCGACAGTACGACACACACACACACAGAGAG	1077
QY	261	TrpLeuGluIleAspLeuGlyLysLysIleThrGlyIleArgThrThrGlySer	280
DB	1078	TGGCTGGAGATCGATTTGGGGGAGAAAAAATAACAGGAATTTAGGACACACAGGATCT	1137
QY	281	ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPhelysAsnAsnAn	300
DB	1138	ACACAGTCGAATCTCAACTTTTATGTTAAGAGTGTGTTGATGAACCTTCAAAACAAATAT	1197
QY	301	SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn	320
DB	1198	TCTAAGTGGAGACCTATTAAGGAATTTGTGAATATTAAGAAAGGTGTTTCAGGGTAAC	1257
QY	321	SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal	340
DB	1258	TCTAATTTTCGGGACCCAGTGCACAAACAATTTTCATCCCTCCCATCGTGGCCAGATATGTG	1317
QY	341	ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys	360
DB	1318	CGGGTTGTCCTCCCGACATGGCACCAGAGGATAGCTTTGAAGGTGGAGCTCATTTGGTTGC	1377


```
Db 718 TATAGAGATACCTCTTATTGTGCAAAAGCTGCCATCCATGCAAGTAATAATTCGTGATGA 777
Qy 161 LeuGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
Db 778 CTAGGTGGCCAGATCAGTGTCTTCAGCGCAAGGATCAGTCGATATGAAGGATCTTG 837
Qy 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
Db 838 GCCAATGGTGTCTTTTCGAGGATGTTCCCTGTGACAGACGATTTCTGTTTACTCTC 897
Qy 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSer 220
Db 898 AATGGTGTGACGACAGATCCTTGTAGTTTGAACCTGACGGGCAATATCAGAGCTTCTCCTCA 957
Qy 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
Db 958 TGGCAGTCGGTCATGAGAGTGAGACCAAGTTTCACTGGTCTCTCGCCAAAGCCCACTT 1017
Qy 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
Db 1018 CAGGACCAAGGCCCATCATGGCTTCGGGCGACAGTAGCAACACCAACACCAAGAG 1077
Qy 261 TrpLeuGluIleAspLeuGlyLysLysLysIleThrGlyIleArgThrThrGlySer 280
Db 1078 TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAATAACAGGAATTAGGACCAACAGGATCT 1137
Qy 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAn 300
Db 1138 ACACAGTCGAACTTCAACTTTTATGTTAAGAGTTTGTGATGAACATTCAAAACATAAT 1197
Qy 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn 320
Db 1198 TCTAAGTGGAGACCTATAAGGAATTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1257
Qy 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
Db 1258 TCTAAGTTCGGGACCCAGTCGAAAAACAATTTTCATCCCTCCCATCGTCCGACAGATATGT 1317
Qy 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
Db 1318 CGGGTGTCCCCAGACATGGCAGCAGGATAGCCTTGAAGTGGAGCTCATTTGGTTGC 1377
Qy 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
Db 1378 CAGATTACACAGGTAATGATTCATTGTTGTGGCGCAACAGTCAAGACCAAGCAGTGT 1437
Qy 381 SerThrLysGlyGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
Db 1438 TCAACTTAAGAAAGAGATGAGACAATCAACAGGCCCATCCCTCGGAAGAAACATCCACA 1497
Qy 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValLeuValPheAla 420
Db 1498 GGAATAAACATTACACGGTGGCTATTCATTGGTGGTCTCTTGTGTCCTGGTGTGTGCT 1557
Qy 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysGlySerProTyrGlySer 440
Db 1558 GGAATGGGATCTTTGCAGCCTTTAGAAAGAGAGAGAAAGAGAGTCCGTATGGATCA 1617
Qy 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
Db 1618 GCAGAGGCTCAGAAACACAGCTGTTGGAAGCAGATTAATATATCCCTTTGCCAGACATCAG 1677
Qy 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
Db 1678 TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAGTTAGATCTTC 1737
Qy 481 IleThrSerAspMetAlaGly 487
Db 1738 ATCACAAGTGATATGCGAGGT 1758
```

RESULT 4
AAS00613

```

ID AC AAS00613;
XX 29-AUG-2001 (first entry)
DE Novel human protein (NHP) DNA sequence #1.
KW Novel human protein; NHP; CUB domain; extracellular domain; gene therapy;
KW obesity; high blood pressure; connective tissue disorder; infertility;
KW NHP-mediated pathway; ds.
XX Homo sapiens.
FH Key Location/Qualifiers
FT CDS 59..1522
FT /*tag= a
FT /product= "Novel human protein #1"
XX WO200129219-A1.
XX 26-APR-2001.
XX 08-OCT-2000; 2000WO-US028798.
XX 19-OCT-1999; 99US-0160285P.
XX 18-FEB-2000; 2000US-0183583P.
XX (LEXI-) LEXICON GENETICS INC.
XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
XX Sands AT;
XX WPI; 2001-290917/30.
XX P-PSDB; AAU00628.
XX Novel nucleic acid encoding human CUB-domain containing protein, useful
XX for drug screening, diagnosis and treatment of physiological disorders or
XX diseases.
XX Disclosure; Page 30-31; 33pp; English.
XX The sequence represents a polynucleotide which encodes a novel human
XX protein (NHP) containing a CUB domain (an extracellular domain). CUB
XX proteins have been associated with regulating development, modulating
XX cellular processes and preventing infectious disease. NHP nucleotide
XX sequences are useful for gene therapy of physiological disorders or
XX diseases. NHP oligonucleotides are useful as hybridisation probes for
XX screening libraries and assessing gene patterns. NHP nucleotide sequences
XX are useful for detecting mutant or inappropriately expressed NHPs (for
XX example, those proteins associated with obesity, high blood pressure,
XX connective tissue disorders and infertility) for the diagnosis of a
XX disease. The polynucleotides may also be used in screening for drugs
XX effective in the treatment of symptomatic or phenotypic manifestations of
XX perturbing the normal function of NHP in the body. Nucleotide constructs
XX encoding NHP products are used to genetically engineer host cells to
XX express such products in vivo. These host calls allow for the
XX identification of compounds that bind to NHP receptors or trigger NHP-
XX mediated pathways
SQ Sequence 1768 BP; 539 A; 370 C; 421 G; 438 T; 0 U; 0 Other;
```

Alignment Scores:

Pred. No.:	4,99e-226	Length:	1768
Score:	2557.00	Matches:	487
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-813-588-2 (1-487) x AAS00613 (1-1768)

Qy 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
AAS00613

Db 59 ATGACATCTAAGAAATATATCCGGGACCTATCCCAATCACATGTTTGGCAAGACAAAT 118
Qy 21 ThrValProLysGlyLysArgLeuLeuLeuAtrGLeuGlyAspLeuAspLeuGlySerGln 40
Db 119 ACGTACCAAGGGGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGNATCCAG 178
Qy 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
Db 179 ACCTGTGCTTCTGACTATCTCTCTTACCAGCTCTTCAGATCAATATGTCCTCACTGT 238
Qy 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
Db 239 GGAAGTATGACTTCTCCCAAGAACTCTTGTGAACACAAAGTGAAGTAAACCGTCCCTTT 298
Qy 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
Db 299 GAGAGTGGATCCCAATTTCTGCCCGGGTTTTTGTGACCTATGCGAGCAGCGACCAT 358
Qy 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
Db 359 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA 418
Qy 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
Db 419 TTTCTGCCACAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 478
Qy 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleLeuAlaAspGlu 160
Db 479 TATAGAGATACCTTCTTTATTTGTGCAAGCTGCTCCATCCATGACAGAAATATGCTGATGA 538
Qy 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
Db 539 CTAGTGGCCAGATCAGTGTGCTTACGCCAAAGGATCAGTCATATGAAGGATTCG 598
Qy 181 AlaAsnGlyValLeuSerArgAspGlySerIleSerAspLysArgPheLeuPheThrSer 200
Db 599 GCCAATGTGTCTTTCTGAGGGATGGTTCTCTGTACAGCAAGGATTTCTGTATCTCC 658
Qy 201 AsnGlyCysSerArgSerLeuSerPheLeuProAspGlyGlnIleArgAlaSerSerSer 220
Db 659 AATGGTTGACGAGATCTTGTAGTTTGAACCTTGACGGGCAATCAGAGCTTCTTCTCA 718
Qy 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
Db 719 TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTCACTGGTCTCTGCGCAAGCCGCACT 778
Qy 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
Db 779 CAGGACCAAGGCCCATCATGCGCTTCGGCGACAGTAGCAACCAACCAACCCAGAG 838
Qy 261 TrpLeuGluIleAspLeuGlyGlyLysLysIleThrGlyIleArgThrThrGlySer 280
Db 839 TGGCTGGAGATCGATTTGGGGGAGAAAGAAATAACAGGATTAGGACCAAGATCT 898
Qy 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
Db 899 ACACAGTCGAACCTTCAACTTTATGTTAAGAGTTTGTGTGAACCTTCAAAAACAATA 958
Qy 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
Db 959 TCTAAGTGGAGACCTTAAGGAATTTGTGAATATGAAGAAAGGTGTTTCAGGGTAAC 1018
Qy 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProPheIleValAlaArgTyrVal 340
Db 1019 TCTAACCTTTGGGACCCAGTGCAGAAACAATTTCACTCCCTCCATCGTGGCCAGATATGT 1078
Qy 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
Db 1079 CGGGTTGTCCCCAGACATGCGACAGAGTAGCTTGAAGGTGGAGCTCATTTGGTGTGC 1138
Qy 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380

Db 1139 CAGATTACACAAAGTAATGATTCAATTGGTGGCGCAAGACAAAGTCAAAAGCACCAGTGT 1198
Qy 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
Db 1199 TCAACTAAGAAAGAGATGAGACAATCAAGGCCCATCCCTCGAAGAAACATCCACA 1258
Qy 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValPheAla 420
Db 1259 GGAATAAACATTACAAACGGTGGCTATTCCATTGGTGCTCTTGTTCCTGGTGTTCCT 1318
Qy 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysLysLysLysLys 440
Db 1319 GGAATGGGATCTTTGACGCTTTTGAAGAAGAAAGAAAGAAAGTCCGTATGGATCA 1378
Qy 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
Db 1379 GCGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAAATATATCCCTTTCAGACATCAG 1438
Qy 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
Db 1439 TCAGCTGAGTTTACCATCAGCTATGATAATGAGAGGAGATGACACAAAAGTTAGATCTC 1498
Qy 481 IleThrSerAspMetAlaGly 487
Db 1499 ATCACAAGTATATGCCAGGT 1519
RESULT 5
ADN39764
ID ADN39764 standard; cDNA; 2010 BP.
XX
AC ADN39764;
XX
17-JUN-2004 (first entry)
XX
Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO: C136.
DE
Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnery; gene therapy; vaccine; gene; ss.
XX
Homo sapiens.
XX
WO2003042661-A2.
XX
22-MAY-2003.
XX
13-NOV-2002; 2002WO-US036810.
XX
13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 23-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-035250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-039775P.
PR 09-SEP-2002; 2002US-0397845P.
XX
09-SEP-2002; 2002US-0409450P.
XX
(SOSB-) BOS BIOTECHNOLOGY INC.
XX

PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
 PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
 XX WPI: 2003-468649/44.
 DR F-PSDB; ADN39981.
 XX
 PT Determining the presence or absence of a pathological cell in a patient,
 PT useful for diagnosing, prognosing or treating cancer, comprises detecting
 PT a nucleic acid in a biological sample.
 XX
 XX Claim 8; SEQ ID NO C136; 1385pp; English.
 XX
 CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
 CC whose expression is upregulated or downregulated in specific cancers or
 CC other diseases such as angiogenic or fibrotic disorders, and to methods
 CC of determining the presence or absence of a pathological cell in a
 CC patient by detecting a nucleic acid at least 80% identical to those of
 CC the invention or by detecting a polypeptide of the invention. The
 CC invention also relates to expression vectors and host cells comprising a
 CC nucleic acid of the invention; antibodies which specifically bind a
 CC polypeptide of the invention; use of such antibodies for drug targeting;
 CC and methods of screening for modulators of activity or expression of the
 CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
 CC antibodies and methods are useful for diagnosing, prognosing and treating
 CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
 CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
 CC neovascularisation syndromes, scarring, and uterine fibroids. They may
 CC also be useful in wound healing and in contraception. The present
 CC sequence represents a nucleic acid sequence of the invention.
 XX
 SQ Sequence 2010 BP; 577 A; 457 C; 512 G; 464 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 5,97e-226 Length: 2010
 Score: 2557.00 Matches: 487
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0
 US-10-813-588-2 (1-487) x ADN39764 (1-2010)
 QY 1 MetThrSerLysAsnThrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
 DB 282 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACACTGTTTCGGAAGAACAAT 341
 QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
 DB 342 ACAGTACCAAGGGGAAAGAGACTGATCTCAGGTTGGAGATTTGGATATCGAATCCAG 401
 QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrProTyrCys 60
 DB 402 ACTGTGCTCTGACTATCTCTCTCCACAGCTCTTCAGATCAATATGGTCCACTACTGT 461
 QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
 DB 462 GGAAGTATGACTGTTCCCAAGAACTCTGTTGGAACACAGTGAAGTACCGTCCGCTTT 521
 QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
 DB 522 GAGAGTGGATCCACATTTCTGCGCGGGGTTTTTTCGTACCTATCGAGCAGCGACCAT 581
 QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
 DB 582 CCAGATTTAATACATGTTTGGAACAGAGCTAGCCATATTATTGAAGACAGATACAGCAAA 641
 QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
 DB 642 TTCTGCGCCAGCTGTTGTAGACGCTAGCAGGAGACATTTCTGGGAAATATGTTAGATGA 701
 QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
 DB 702 TATAGAGATACCTCTTTATTGTGCAAGAGCTGCCATCCATCGAGGAATAATTGCTGATGAA 761

QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
 DB 762 CTAGGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGATCAGTCGATATGAAGGATCTG 821
 QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
 DB 822 GCCAATGGTGTCTTTTCGAGGGATGTTCCCTGTGCAGACAAGGATTTCTGTGTACCTCC 881
 QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
 DB 882 AATGGTTGCAGCAGATCCTTGAGTTTGAACCTGACGGCAATCAGAGCTTCTTCCTCA 941
 QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
 DB 942 TGGCAGTCGGTCAATGAGAGTGAGACCAAGTTCTCTGTCTCTCGCCCAAGCCGACTT 1001
 QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
 DB 1002 CAGGACCAAGGCCCATCATGGCTTCGGCGCAGTAGCAACAACCAACACACGAGAG 1061
 QY 261 TrpLeuGluIleAspLeuGlyGluLysLysLysIleThrGlyIleArgThrGlySer 280
 DB 1062 TGGCTGGAGATCGATTTGGGGGAGAAAAAATAACAGGAATTAGGACCCACAGGATCT 1121
 QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
 DB 1122 ACACATCGAATCTTCACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAACAATAAT 1181
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 DB 1182 TCTAAGTGAAGACCTATAAGGAATTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1241
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 DB 1362 CAGATTTACACAAGGTAATGATTTTCATTTGTTGGCGCAGACAAGTCAAAAGCACCACTGTT 1421
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 DB 1422 TCAACTTAAGAAAGAGATGAGACAATCAACAAGGCCCATCCCTCGGAAGAAACATCCACA 1481
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 DB 1542 GCAATGGGCGATCTTTGCGAGCCCTTAGAAAGAAAGAAAGAAAGAAAGTCCGATGATCA 1601
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 DB 1602 GCAGAGGCTCAGAAAAACAGACTGTTTGAAGACAGATTTAAATATATCCCTTTGCCAGACATCAG 1661
 QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
 DB 1662 TCAGCTGAGTTTACCATTCAGCTATGATATGAGAGAGATGACACAAAGTTAGATCTC 1721
 QY 481 IleThrSerAspMetAlaGly 487
 DB 1722 ATCACAAGTGATATGCGAGGT 1742
 RESULT 6
 ID ADR46610
 ID ADR46610 standard; DNA; 2010 BP.
 XX

AC ADR46610;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Cancer-associated protein coding sequence, SEQ ID 23.
 XX
 KW Cytostatic; Gene Therapy; cancer; human; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 126..1745
 FT /tag= a
 FT /product= "Cancer-associated protein, SEQ ID 81"
 FT
 PN WC2004073657-A2.
 XX
 PD 02-SEP-2004.
 XX
 PF 19-FEB-2004; 2004WO-US005455.
 XX
 PR 19-FEB-2003; 2003US-0448784P.
 XX
 PA (PROT-) PROTEIN DESIGN LABS INC.
 XX
 PI Aziz N, Gish KC, Wilson KE, Zlotnik A;
 XX
 DR WPI; 2004-652787/63.
 DR P-PSDB; ADR4668.
 XX
 PT Detecting a pathological cell in a patient for diagnosing or treating
 PT cancer by detecting in a biological sample from the patient genes whose
 PT expression are up-regulated or down-regulated in specific cancers.
 XX
 PS Claim 1; SEQ ID NO 23; 375pp; English.
 XX
 CC The present invention relates to a method for detecting cancer in a
 CC patient. The method comprises detecting in a biological sample from the
 CC patient a nucleotide or protein sequence comprising a sequence that is at
 CC least 80% identical to a nucleotide sequence (ADR46588-ADR46645) or
 CC protein sequence (ADR46646-ADR46703). The method is useful for detecting
 CC cancer for preparing a composition for diagnosing or treating cancer.
 XX
 SQ Sequence 2010 BP; 577 A; 457 C; 512 G; 464 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 5,97e-226 Length: 2010
 Score: 2557.00 Matches: 487
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0
 US-10-813-588-2 (1-487) x ADR46610 (1-2010)
 Qy 1 MetThrSerLysAenTyrProGlyThrTyrProAenHisThrValCysGluLysThre 20
 Db 282 ATGACATCTAAGAAATTATCCGGACCTACCCCAATCACACTGTTTCGAAAAGACAATT 341
 Qy 21 ThrValProLysGlyLysArgLeuLeileuArgLeuGlyAspLeuAspLeuGln 40
 Db 342 ACAGTACCAAGGGGAAAGAACTGATCTGAGGTGGGAGATTGGATATCGAATCCAG 401
 Qy 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
 Db 402 ACCGTGCTTCTGACTATCTCTTCCAGCTCTTCAGATCAATATGGTCCATCTGT 461
 Qy 61 GlySerMetThrValProLysGluLeuLeuAenThrSerGluValThrValArgPhe 80
 Db 462 GGAAGTATGACTGTTCACAAAGAACTCTTGTGGAACAACAGTGAAGTAACCGTCCGCTTT 521
 Qy 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
 |||

Db 522 GAGGTGGATCCACATTTCTGCGCGGGGTTTTTGTGCTGACCTATGCGAGCGACCAT 581
 Qy 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
 |||
 Db 582 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA 641
 Qy 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAenMetValAspGly 140
 |||
 Db 642 TTCTGCCAGCTGGTTGTAGACAGTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 701
 Qy 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyLysIleLeuAspGlu 160
 |||
 Db 702 TATAGAGATACCTCTTTATTTGCAAGCTGCCATCCATCGCAGAAATATTTGCTGATGA 761
 Qy 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
 |||
 Db 762 CTAGGTGGCCAGATCAGTGTCTTCAGCGCAAGGGATCAGTCGATATGAAGGATTTCTG 821
 Qy 181 AlaAenGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
 |||
 Db 822 GCCAATGGTGTCTTTTCGAGGGATGGTTCCTGTTCAGCAAGCGATTTCTGTTTACTCTC 881
 Qy 201 AenGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
 |||
 Db 882 AATGTTTGACGACGATCCTTGATTTTGAACTGACGGGCAATCAGAGCTTCTTCTCTCA 941
 Qy 221 TrpGlnSerValAenGluSerGlyAspGlnValHisTyrPsrProGlyGlnAlaArgLeu 240
 |||
 Db 942 TGGCACTCGGTCAATGAGAGTGGAGACCAAGTTTCACTGGTCTCTGCGCAAGCCGACTT 1001
 Qy 241 GlnAenGlnGlyProSerTrpAlaSerGlyAspSerSerAenAenHisLysProArgGlu 260
 |||
 Db 1002 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACCAACCAACACAGAG 1061
 Qy 261 TrpLeuGluIleAspLeuGlyGluLysLysLysIleThrGlyIleArgThrGlySer 280
 |||
 Db 1062 TGCTCGAGATCGATTTGGGGAGAAAAGAAATTAACAGGAATTAGGACCACAGATCT 1121
 Qy 281 ThrGlnSerAenPheAenPheTyrValLysSerPheValMetAenPheLysAenAenAgn 300
 |||
 Db 1122 ACACAGTCGAACCTTCAACTTTTATGATGAGTGTGTGATGAACCTTCAAAAACAATAAT 1181
 Qy 301 SerLysTrpLysThrTyrLysGlyIleValAenAenGluLysValPheGlnGlyAen 320
 |||
 Db 1182 TCTAAGTGGAAAGACCTATAAAGGAATGTGAATTAATGAAGAAAGGTTTTCAGGGTAAC 1241
 Qy 321 SerAenPheArgAspProValGlnAenAenPheIleProProIleValAlaArgTyrVal 340
 |||
 Db 1242 TCTAATCTTCGGACCCAGTCGAAAACAATTTTCATCCCTCCATCGTGGCCAGATATGTG 1301
 Qy 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
 |||
 Db 1302 CGGGTTGTCCCCAGACATGGCACAGAGATAGCTTGAAGGTGGAGCTCAITGGTTGC 1361
 Qy 361 GlnIleThrGlnGlyAenAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
 |||
 Db 1362 CAGATTACACAGGTAAATGATTCATTTGGTGTGGCGAAGCAAGTCAAGACACCGATGTT 1421
 Qy 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
 |||
 Db 1422 TCACTTAAGAAAGAGATGAGACATCACAAAGGCCCATCCCTCGGAAGAAACATCCACA 1481
 Qy 401 GlyIleAenIleThrThrValAlaIleProLeuValLeuLeuValValLeuValPheAla 420
 |||
 Db 1482 GGAATAAACATTAACAACGGTGGCTATTTCATTTGGTGTCTCTTGTGTCTCTGTTTGTCT 1541
 Qy 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysGlySerProTyrGlySer 440
 |||
 Db 1542 GGAATGGGATCTTTTCAGGCTTTTAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1601
 Qy 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
 |||
 Db 1602 GCAGAGGCTCAGAAAACAGACTGTGGAAGCAGATTAATATCCCTTTGCGACAGATCAG 1661

QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
|||||
Db 1662 TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAGTTAGATCTC 1721
QY 481 IleThrSerAspMetAlaGly 487
|||||
Db 1722 ATCACAAGTGATATGCCAGGT 1742

RESULT 7

ADR46611

ID ADR46611 standard; DNA; 2010 BP.

XX

AC ADR46611;

XX

DT 18-NOV-2004 (first entry)

XX

DE Cancer-associated protein coding sequence, SEQ ID 24.

XX

KW Cytostatic; Gene Therapy; cancer; human; gene; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 136..1745

FT /tag= a

FT /product= "Cancer-associated protein, SEQ ID 82"

XX

PN WO2004073657-A2.

XX

PD 02-SEP-2004.

XX

PF 19-FEB-2004; 2004WO-US005455.

XX

PR 19-FEB-2003; 2003US-0448784P.

XX

PA (PROT-) PROTEIN DESIGN LABS INC.

XX

PI Aziz N, Gish KC, Wilson KE, Zlotnik A;

XX

DR WPI: 2004-652787/63.

XX

DR P-PSDB; ADR46669.

XX

PT Detecting a pathological cell in a patient for diagnosing or treating

XX

PT cancer by detecting in a biological sample from the patient genes whose

XX

PT expression are up-regulated or down-regulated in specific cancers.

XX

PS Claim 1; SEQ ID NO 24; 375pp; English.

XX

CC The present invention relates to a method for detecting cancer in a

XX

CC patient. The method comprises detecting in a biological sample from the

XX

CC patient a nucleotide or protein sequence comprising a sequence that is at

XX

CC least 80% identical to a nucleotide sequence (ADR46588-ADR46645) or

XX

CC protein sequence (ADR46646-ADR46703). The method is useful for detecting

XX

CC cancer for preparing a composition for diagnosing or treating cancer.

XX

SQ Sequence 2010 BP; 577 A; 457 C; 512 G; 464 T; 0 U; 0 Other;

XX

Alignment Scores:

Pred. No.: 5.97e-226 Length: 2010

Score: 2557.00 Matches: 487

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 13 Gaps: 0

US-10-813-588-2 (1-487) x ADR46611 (1-2010)

QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20

Db 282 ATGACATCTAAGAAATATCCGGACCTACCCCAATACACACTGTTTGGCAAGACAAT 341

QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40

Db 342 ACAGTACCAAGGGGAAAAGACTGATTCCTGAGTTGGAGATTGTCATATCGAATCCCAG 401
QY 41 ThrCysAlaSerAspTyrIleuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
Db 402 ACCTGTGCTTCTGACTATCTTCTCTTCCACAGCTCTTCCAGATCAATATGGTCCATCTGT 461
QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
Db 462 GGAAGTATGACTGTTCCCAAGACTCTTGTGTAACACAAGTGAAGTACCGTCCGCTTT 521
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuLeuThrTyrAlaSerSerAspHis 100
Db 522 GAGAGTGGATCCACATTTCTGCCCGGGGTTTTTGTGCTGACCTATCGGAGCAGCACCAT 581
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
Db 582 CCAGATTTAATAACATGTTTGAACGAGCTAGCTATTATTGAAGACAGAAATACAGCAA 641
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
Db 642 TTCTGCCAGCTGGTTGTAGACAGCTAGCAGGAGACATTTCTGGGAATATGGTAGTGA 701
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
Db 702 TATAGAGATACCTCTTTATTGTGCAAGCTGCCATCCATGCAGGAATAATTGCTGATGAA 761
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
Db 762 CTAGGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATGAAGGATTTCTG 821
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
Db 822 GCCAATGGTGTCTTTTCAGGGATGGTTCCTGTTCAGACAGCGATTTCTGTTTACTCC 881
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
Db 882 AATGGTTGCAGCAGATCCTTGAGTTTGAACCTGACGGGCAAAATCAGAGCTTCTTCTCA 941
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
Db 942 TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTCACTGTCTCTCGGCAAGCCCACTT 1001
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
Db 1002 CAGGACCAAGGCCCATCATGGCTTCGGCGGACAGTAGCAACACCAACACACAGAG 1061
QY 261 TrpLeuGluIleAspLeuGlyGluLysLysIleThrGlyIleArgThrThrGlySer 280
Db 1062 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAAGATCT 1121
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
Db 1122 ACACAGTCGAACCTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAACAATA 1181
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
Db 1182 TCTAAGTGAAGACCTTAAAGGAATTGTGATATATGAAGAAAGGTGTTTCAGGGTAC 1241
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
Db 1242 TCTAACTTTGGGAGCCAGTGCAAAACAATTTTCATCCCTCCCATCGTGCCAGATATGTG 1301
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
Db 1302 CGGGTTGTCCCCCAGACATGGCAGGATAGCTTGAAGGTGGAGCTCATTTGTTGTC 1361
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
Db 1362 CAGATTACACAGGTAAATGATTCATTTGGTGTGGCGCAGACAAAGTCAAGACCACTGTT 1421
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400

QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
Db 637 CTAGGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATGAGGGATTCTG 696
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
Db 697 GCCAATGGGTGCTTTTCGAGGATGGTTCCTGTCCAGACAAGCGATTTCTGTGTACCTCC 756
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
Db 757 ATGGTGTGACGACAGATCTTGTAGTTTGAACCTGACGGCAATACAGAGCTTCTTCTCA 816
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValIleTrpSerProGlyGlnAlaArgLeu 240
Db 817 TGGCAGTGGTCAATGAGAGTGAGACCAAGTTCACTGGTCTCTGGCCCAAGCCGACTT 876
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
Db 877 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACAACCAACACGAGAG 936
QY 261 TrpLeuGluIleAspLeuGlyGlyLysLysLysIleThrGlyIleArgThrThrGlySer 280
Db 937 TGGCTGGAGATCATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAAGGATCT 996
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsnAsn 300
Db 997 ACACAGTCGAACCTTCAACTTTTATGTTTAAAGATTTTGTGATGAATTTCAAAAACAATAAT 1056
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
Db 1057 TCTAAGTGAAGACCTATAAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGGTAAC 1116
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProPheValAlaArgTyrVal 340
Db 1117 TCTAAGTGGGACCCAGTGCACAAACAATTTCTCCCTCCCATCGTGGCCAGATATGG 1176
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
Db 1177 CGGGTTGTCCTCCCGACATGGCCACGAGAGATAGCTTGAAGGTGGAGCTCATTTGTTGC 1236
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
Db 1237 CAGATTACACAGGTAAATGATTCATTTGGTGTGGCGCAAGCAAGTCAAAAGCACCACTGTT 1296
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
Db 1297 TCAACTAAGAAAGAGATGAGACAAATCAAGAGCCCATCCCTCCGGAAGAAACATCCACA 1356
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValPheAla 420
Db 1357 GGAATAAACATTACAACGGTGGCTATTCATTGGTCTCTTGTCTGCTGGTGTGCT 1416
QY 421 GlyMetGlyIlePheAlaPheArgLysLysLysLysGlySerProTyrGlySer 440
Db 1417 GGAATGGGATCTTTTCAGCCTTTAGAAAGAAAGAAAGAAAGTCCGTATGATCA 1476
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
Db 1477 GCAGAGGCTCAGAAACAGACTGTTGGAAGCAGATTAATATATATATATATATATATATAT 1536
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
Db 1537 TCAGCTGAGTTTACCATCAGCTATGATATAGAGAGAGATGACACAAAGATTAGATCTC 1596
QY 481 IleThrSerAspMetAla 486
Db 1597 ATCAAGAATGATAGGCA 1614

RESULT 9

ADQ10135

ID ADQ10135 standard; cDNA; 2145 BP.

XX AC

ADQ10135;

XX 09-SEP-2004 (first entry)
XX Human polynucleotide #11.
XX Human; gene; ss; cancer; obesity; gastritis; diarrhea; haemorrhoid;
KW asthma; anaemia; graft-versus-host reaction; allergic reaction;
KW cystic fibrosis; hypogonadism; cardiovascular disorder; arthritis;
KW osteoarthritis; arteriosclerosis; hypertension; bacterial infection;
KW peptic ulcer; diabetes mellitus; hepatitis; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; AIDS; tuberculosis;
KW viral infection; malaria; goiter; infertility; endometriosis;
KW muscular disorder.
XX Homo sapiens.
XX US2004121396-A1.
XX 24-JUN-2004.
XX 19-DEC-2003; 2003US-00741790.
XX 14-JUN-1999; 99US-00333159.
XX 29-JUN-1999; 99US-00342364.
XX 10-SEP-1999; 99US-00393996.
XX 19-OCT-1999; 99US-00420707.
XX 07-JAN-2000; 2000US-00479249.
XX 27-APR-2000; 2000US-00559497.
XX 24-MAY-2000; 2000US-00578063.
XX 16-JUN-2000; 2000US-00596194.
XX 23-JUN-2000; 2000US-00602871.
XX 30-JUN-2000; 2000US-00608452.
XX 12-JAN-2001; 2001US-00759130.
XX (MILL-) MILLENNIUM PHARM INC.
XX Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;
PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADU;
XX WPI; 2004-479675/45.
XX New TANGO, INTERCEPT, and MANGO, useful in diagnosing, preventing, and
PT treating cancer, constipation, hemorrhoids, cystic fibrosis,
PT hypogonadism, psoriasis, hepatitis, Alzheimer's disease, AIDS,
PT tuberculosis, malaria, goiter, infertility.
XX Claim 2; SEQ ID NO 72; 483pp; English.
XX The invention relates to human polynucleotides and the polypeptides they
CC encode. The invention also relates to a host cell containing a
CC polynucleotide of the invention, an antibody which selectively binds with
CC a polypeptide of the invention, a method of detecting the presence of a
CC polypeptide in a sample, a method of identifying a compound which binds
CC with a polypeptide, and a method of modulating the activity of a
CC polypeptide. The polynucleotides, polypeptides and compositions are
CC useful for diagnosing, preventing and/or treating cancer, obesity,
CC gastritis, diarrhea, haemorrhoids, asthma, anaemia, graft-versus-host
CC reactions, allergic reactions, cystic fibrosis, hypogonadism,
CC cardiovascular disorders, arthritis, osteoarthritis, arteriosclerosis,
CC hypertension, bacterial infections, psoriasis, diabetes mellitus,
CC hepatitis, Alzheimer's disease, Huntington's disease, Parkinson's
CC disease, AIDS, tuberculosis, viral infections, malaria, goiter,
CC infertility, endometriosis, wounds and muscular disorders. This sequence
CC represents a human polynucleotide of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification but
CC was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX SQ Sequence 2145 BP; 556 A; 561 C; 575 G; 453 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,34e-225 Length: 2145

Score: 2551.00 Matches: 486

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.77%	Indels:	0
DB:	12	Gaps:	0

US-10-813-588-2 (1-487) x ADQ10135 (1-2145)			
QY	1	MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGlyLysThrIle	20
DB	157	ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACACTGTTTGGCAAGAACAAAT	216
QY	21	ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln	40
DB	217	ACAGTACCAAGGGGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCCG	276
QY	41	ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys	60
DB	277	ACCTGTGCTTCTGACTATCTTCTTCCAGGCTCTTCAGATCATATGTCATACTGT	336
QY	61	GlySerMetThrValProLysGluLeuLeuAsnThrSerGluValThrValArgPhe	80
DB	337	GGAAGTATGACTCTTCCAAAGAACTCTTGTTCAACACAAAGTGAAGTAAACCGTCCGCTT	396
QY	81	GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis	100
DB	397	GAGAGTGGATCCACATTTCTGGCGGGGTTTTTGTGACCTATTCGAGCAGCGACCAT	456
QY	101	ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys	120
DB	457	CCAGATTAAATACATGTTTGGAAACGAGCTAGGCATTAATTTGAAGACAGATACAGCAA	516
QY	121	PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly	140
DB	517	TTCTGCCACGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGAAATATGGTAGATGA	576
QY	141	TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisIleGlyIleLeuAlaAspGlu	160
DB	577	TATAGATACCTCTTTATTTGTCAAGCTGCCATCCATCCAGGAATAATTTCTGTATGAA	636
QY	161	LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu	180
DB	637	CTAGGTGGCAGATCAGTGTCTTCAGCGCAAGGATTCAGTCGATGATGAAGGATCTG	696
QY	181	AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer	200
DB	697	GCCAAATGGTGTCTTTTCAGGAGTGGTTCCTGTGCAGCAAGCAATTTCTGTATACCTCC	756
QY	201	AsnGlyCysSerArgSerLeuPheGluProAspGlyGlnIleArgAlaSerSerSer	220
DB	757	ANTGGTTGCCAGCATCTTGAGTTTTTGAACCTGACGGGCAATTCAGAGCTTCTTCTCA	816
QY	221	TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu	240
DB	817	TGGCAGTCCGTCAATGAGATGGAGACCAAGTTCACTGGTCTCTGCGCAAGCCGACTT	876
QY	241	GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnHisLysProArgGlu	260
DB	877	CAGGACCAAGGCCCATCATGGCTTCGGCGCACAGTAGCAACACCAACCAACACAGAG	936
QY	261	TrpLeuGluLeuAspLeuGlyGlyLysValLysIleThrGlyIleArgThrThrGlySer	280
DB	937	TGGCTGGAGATCGAATTTGGGGGAGAAAAGAAATAACAGAAATTAGGACACAGGATCT	996
QY	281	ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn	300
DB	997	ACACGTGCAACTTCACTTTATTTAGTAAAGTTTGTGATGACTTCAAAACAAATAT	1056
QY	301	SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn	320
DB	1057	TCTAAGTGAAGACCTATAAGGAATTTGTGAATTAATGAAGAAAGGTGTTTCAGGGTAA	1116
QY	321	SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal	340

Db	1117	TCTAACTTTCGGGACCCAGTGCAAAACAATTTTCATCTCCCTCCCATCGTGCCAGATATGTG	1176
QY	341	ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLeuValGluLeuLeuGlyCys	360
DB	1177	CGGGTTGTCCCCAGACATGGCACAGAGGATAGCTTTGAAGGTGGAGCTCATTTGTTGC	1236
QY	361	GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal	380
DB	1237	CAGATTACACAAGGTAAATGATTCATTGGTGTGGCCCAAGACAAGTCAAGACCAAGTGT	1296
QY	381	SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr	400
DB	1297	TCAACTAAGAAAGATGAGACAATCAACAGGCCATCCCTCGGAAGAAACATCCACA	1356
QY	401	GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValPheAla	420
DB	1357	GGATAAACAATTAACAACGGTGGCTATTCATTGGTGTCTTGTGTTCTGTTGTTGCT	1416
QY	421	GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysGlySerProTyrGlySer	440
DB	1417	CGAATGGGATCTTTTCAGACCTTTAGAAGAAAGAAAGAAAGAGAGTCCGTATGATCA	1476
QY	441	AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln	460
DB	1477	GCAGAGCTCAGAAACACAGCTGTTGGAAGCAGATTAAATATCCCTTTGCCAGACATCAG	1536
QY	461	SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu	480
DB	1537	TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAAGTTAGATCTC	1596
QY	481	IleThrSerAspMetAla	486
DB	1597	ATCAAGTGTATGGCA	1614

RESULT	10
AD128055	
ID	AD128055 standard; cDNA; 2888 BP.
XX	
AC	AD128055;
XX	
DT	15-APR-2004 (first entry)
XX	
DE	ECMAD gene clone 184661CB1.
XX	
KW	db; gene; nootropic; antisickling; antianemic; antitumor; anti-HIV;
KW	antiallergic; antianemic; antiasthmatic; immunosuppressive;
KW	antithrombotic; dermatological; nephrotrophic; antigout;
KW	antichondrocytic; neuroprotective; osteopathic; antipeptidic; antirheumatic;
KW	antiarthritic; antiulcer; antiinflammatory; ophthalmological;
KW	anticonvulsant; antiparkinsonian; antibacterial; virucide; tranquilizer;
KW	neuroleptic; antidiabetic; cytostatic; hepatotrophic; gene therapy;
KW	human extracellular matrix and cell adhesion molecule; ECMAD; diagnosis;
KW	genetic disorder; adrenoleukodystrophy; Down's syndrome; cystic fibrosis;
KW	Gaucher's disease; myotonic dystrophy; sickle cell anemia; thalassemia;
KW	Wilms' tumor; immunological disorder; acquired immunodeficiency syndrome;
KW	AIDS; adult respiratory distress syndrome; allergy; anemia; asthma;
KW	atherosclerosis; autoimmune hemolytic anemia; contact dermatitis;
KW	Goodpasture's syndrome; gout; Grave's disease; multiple sclerosis;
KW	osteoporosis; psoriasis; rheumatoid arthritis; scleroderma;
KW	systemic lupus erythematosus; ulcerative colitis; uveitis;
KW	neurological disorder; epilepsy; stroke; Alzheimer's disease;
KW	Huntington's disease; Parkinson's disease; multiple sclerosis;
KW	meningitis; periodic paralysis; mental disorder; mood; anxiety;
KW	schizophrenia; amnesia; diabetic neuropathy; connective tissue disorder;
KW	osteoporosis; Paget's disease; osteonecrosis; osteomyelitis;
KW	chondrosarcoma; giant cell tumor; psoriatic arthritis;
KW	infectious arthritis; systemic sclerosis; cell proliferative disorder;
KW	actinic keratosis; atherosclerosis; hepatitis; psoriasis; cancer;
KW	adenocarcinoma; leukemia; lymphoma; melanoma; myeloma.
OS	Homo sapiens.
XX	
PN	W0200202634-A2.

XX

PD 10-JAN-2002.

XX

PF 29-JUN-2001; 2001WO-US021067.

XX

PR 30-JUN-2000; 2000US-0215454P.

PR

PR 18-JUL-2000; 2000US-0219462P.

PR

PR 12-OCT-2000; 2000US-0240106P.

PR

PR 12-OCT-2000; 2000US-0240111P.

PR

PR 27-OCT-2000; 2000US-0244021P.

PR

PR 14-NOV-2000; 2000US-0248887P.

PR

PR 16-NOV-2000; 2000US-0249570P.

XX

(INCY-) INCYTE GENOMICS INC.

XX

Tang YT, Yue H, Azimzai Y, He A, Batra S, Lo TP, Nguyen DB;
 Burdill JD, Marcus GA, Zingler KA, Gandhi AR, Lal P, Kearney L;
 Burford N, Yao MG, Walla NK, Elliot S, Patterson C, Khan FA;
 Baughn MR, Hafalia AJA, Policky JL, Au-Young J, Lu Y, Borowsky ML;
 Lu DAM, Ramkumar J, Yang J, Gururajan R, Warren BA, Gietzen K;
 Xu Y, Kallick DA, Lee EA, Thangavelu K, Delegeane AM, Lee S;
 WPI; 2002-154732/20.
 P-PSDB; ADI28019.

DR

Novel isolated human extracellular matrix and cell adhesion molecules
 useful for treating, preventing connective tissue disorder e.g.
 osteoporosis, Paget's disease, genetic disorder e.g. cystic fibrosis,
 thalassemia.

XX

PS Claim 11; SEQ ID NO 47; 270pp; English.

XX

The invention relates to a novel isolated human extracellular matrix and
 cell adhesion molecule (referred to as ECMAD 1-36), its biologically
 active or immunogenic fragment or a sequence comprising 90 % identity to
 ECMAD 1-36. The molecule is useful for screening a compound for
 effectiveness as agonist or antagonist of itself. The protein and its
 encoding nucleic acid are useful in the diagnosis, treatment and
 prevention of genetic disorder such as adrenoleukodystrophy, Down's
 syndrome, cystic fibrosis, Gaucher's disease, myotonic dystrophy, sickle
 cell anemia, thalassemia, Wilms' tumor, etc., immunological disorders such
 as acquired immunodeficiency syndrome (AIDS), adult respiratory distress
 syndrome, allergies, anemia, asthma, atherosclerosis, autoimmune
 hemolytic anemia, contact dermatitis, Goodpasture's syndrome, gout,
 Grave's disease, multiple sclerosis, osteoporosis, psoriasis, rheumatoid
 arthritis, scleroderma, systemic lupus erythematosus, ulcerative colitis,
 arthritis, etc., a neurological disorder such as epilepsy, stroke,
 Alzheimer's disease, Huntington's disease, Parkinson's disease, multiple
 sclerosis, bacterial and viral meningitis, periodic paralysis, mental
 disorders including mood, anxiety, and schizophrenic disorders, amnesia,
 diabetic neuropathy, etc., connective tissue disorder such as
 osteoporosis, Paget's disease, osteonecrosis, osteomyelitis,
 chondrosarcoma, giant cell tumor, psoriatic arthritis, infectious
 arthritis, systemic sclerosis, etc., and a cell proliferative disorder
 such as actinic keratosis, atherosclerosis, hepatitis, psoriasis, cancers
 including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, etc.

CC

This sequence represents the cDNA sequence encoding one of the novel
 proteins.

CC

XX

SQ

Sequence 2888 BP; 736 A; 696 C; 775 G; 681 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3 56e-225 Length: 2888
 Score: 2551.00 Matches: 486
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.77% Indels: 0
 DB: 6 Gaps: 0

XX

SQ

XX

XX

XX

XX

XX

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XX

XX

XX

XX

XX

XX

XX

QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
 DB 1422 TCAACTAAGAAAGAGATGAGACAATCACAAAGGCCATCCCTCGGAAGAAACATCCACA 1481
 QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValIleValPheAla 420
 DB 1482 GGAATAAACATTAACAAGGGGTATTCATTTGGTGTCTCTTGTCTGGGTGTGTCT 1541
 QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysGlySerProTyrGlySer 440
 DB 1542 GGAATGGGATCTTTGCGAGCTTTAGAAAGAGAGAGAGAGAGAGAGAGAGATCGATGATCA 1601
 QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
 DB 1602 GCAGAGGCTCAGAAACACAGACTGTGGAAGCAGATTAAATATATCCCTTTCGACACATCAG 1661
 QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
 DB 1662 TCAGCTGAGTTTACCATCAGCTATGATATATGAGAGGAGATGACACAAAAGTTAGATCTC 1721
 QY 481 IleThrSerAspMetAla 486
 DB 1722 ATCACAAGTGATATGGCA 1739

RESULT 11

ABN86493
 ID ABN86493 standard; cDNA; 3151 BP.

AC ABN86493;

DT 21-OCT-2002 (first entry)

XX Human neurophilin homologue polypeptide, zcub5 encoding cDNA.

XX Neurophilin; zcub5; human; antitumor; antidiabetic; ophthalmological;
 KW antithrombotic; antipsoriatic; antirheumatic; antidiabetic; gene;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW cytosolic; gene therapy; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH 76..2223
 FT /*tag= a
 FT /product= "zcub5"

XX WO200253739-A2.

XX 11-JUL-2002.

XX 15-NOV-2001; 2001WO-US045542.

XX 15-NOV-2000; 2000US-0249004P.

XX (ZYMO) ZYMOGENETICS INC.

XX Fox BA, Gao Z, Shoemaker KE;

XX WPI, 2002-590634/63.

XX P-PSDB; ABB81000.

XX Novel isolated neurophilin homolog polypeptide, termed zcub5, useful in
 PT diagnosis or treatment of disorders associated with abnormal cell
 PT proliferation such as cancer and diseases of the nervous system.

XX Example 2; Page 72-77; 101pp; English.

XX The invention relates to an isolated neurophilin homologue polypeptide,
 CC termed zcub5. The polypeptide can be expressed by standard recombinant
 CC methodology. The zcub5 polypeptide and polynucleotide are useful in a
 CC variety of therapeutic, diagnostic and research applications. The
 CC polypeptide is useful for producing antibodies, for imaging tumours or

CC other sites of abnormal cell proliferation, for treating solid tumours,
 CC retinopathies (including diabetic retinopathy and macular degeneration),
 CC atherosclerosis, psoriasis, rheumatoid arthritis and growth factor-
 CC dependent pathologies, to design agonists and antagonists of neurophilin
 CC -senaphorin interactions, for repairing neurological damage due to
 CC stroke, head and spinal injuries, for treating neurodegenerative diseases
 CC such as multiple sclerosis, Alzheimer's disease, and Parkinson's disease,
 CC for mediating development and innervation of stomach tissue, for
 CC identifying, labeling, and isolating selected cell types, as a target for
 CC cell-specific delivery of diagnostic and therapeutic agent, and to
 CC identify inhibitor of zcub5 activity. The zcub5 polypeptide,
 CC polynucleotide and modulators are useful in diagnosis or treatment of
 CC disorders associated with abnormal cell proliferation, including cancer,
 CC impaired or excessive vasculogenesis or angiogenesis and diseases of the
 CC nervous system. The present sequence represents a cDNA encoding the human
 CC zcub5 polypeptide

XX
 SQ Sequence 3151 BP; 832 A; 752 C; 824 G; 743 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4,02e-225 Length: 3151
 Score: 2551.00 Matches: 486
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.77% Indels: 0
 DB: 6 Gaps: 0

US-10-813-588-2 (1-487) x ABN86493 (1-3151)

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 DB 232 ATGACATCTAAGAAATATATCCCGGACCTACCCCAATCACACTGTTTGGGAAAGACATTT 231
 QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
 DB 292 ACAGTACCAAGGGAAGAGACTGATTCTGAGTTGGAGATTTGGATATCGAATCCAG 351
 QY 41 ThrCysAlaSerAspTyrIleuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
 DB 352 ACCTGTGCTTCTGACTATCTCTCTTCCACAGCTCTTCAGATCAATATGATGTCATACTGT 411
 QY 61 GlySerMetThrValProLysGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
 DB 412 GGAAGTATGACTGTTCCCAAGAACTCTTGTGACACAAAGTGAAGTAACCGTCCGCTTT 471
 QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuLeuThrTyrAlaSerSerAspHis 100
 DB 472 GAGAGTGGATCCACATTTCTGGCCGGGTCTTCTGCTGACCTATGCGAGCAGCGACCAT 531
 QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
 DB 532 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACAGCAA 591
 QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
 DB 592 TTCTGCCAGCTGGTTGTAGACAGTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 651
 QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
 DB 652 TATAGAGATACCTCTTTTATTGTGCAAAAGCTGCCATCCATGCGAGGAATAATTTGCTGTAA 711
 QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
 DB 712 CTAGGTGGCCAGATCATGTGTCTTCAGCGCAAGGAGTCAAGTCATATGAAGGATTTCTG 771
 QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
 DB 772 GCCAATGGTGTCTTTTCGAGGGATGGTTCCCTGTCAGCAAGCGAATTTCTGTTACCTCC 831
 QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
 DB 832 AATGGTTGCAGACATCTTGTAGTTTTGAACCTGACGGGCAATTCAGAGCTTCTTCTCTCA 891

```
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 892 TGGCAGTCGTCAATGAGATGGAGACCAAGTTCACTGGTCTCTGCGCCAGCCGACTT 951
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 952 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACAACACCAAAACCAGAG 1011
QY 261 TrpLeuGluIleAspLeuGlyGluLysLysLysLysLysLysLysLysLysLysLys 280
DB 1012 TGGCTGGAGATCGATTTGGGGGAGAAAAAATAACAGGAATAGGACCAAGATCT 1071
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
DB 1072 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTTTGTGATGAACCTTCAAAA 1131
QY 301 SerLysTrpLysTrpLysGlyLysLysLysLysLysLysLysLysLysLysLys 320
DB 1132 TCTAAGTGGAGACCTATAAAGGAAATTTGTAATAATGAAGAAAGGTGTTTCAGG 1191
QY 321 SerAsnPheArgAspProValGlnAsnAsnAsnPheIleProProIleValAlaArg 340
DB 1192 TCTAAGTGGAGACCTATAAAGGAAATTTGTAATAATGAAGAAAGGTGTTTCAGG 1251
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGly 360
DB 1252 CGGGTTGTCCTCCAGACATGGCCAGACAGAGATAGCCTTGAAGGTGGAGCTCAT 1311
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSer 380
DB 1312 CAGATTACACAAGGTAATGATTCATTTGGTGTGGCGCAGACAAAGTCAAAAGC 1371
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSer 400
DB 1372 TCACTAAGAAAGAGATGAGCAATCAAGGCCCTCCCTCGGAAGAAATCCACA 1431
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValPheAla 420
DB 1432 GGAATAAATACATTACACGGTGGCTATTCCATTGGTGTCTCTTGTCTGGTGTG 1491
QY 421 GlyMetGlyIlePheAlaIleAlaPheArgLysLysLysLysLysLysLysLys 440
DB 1492 GGAATGGGATCTTTGCAGCCTTTAGAAAGAAAGAAAGAAAGAAAGTCCGTATG 1551
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHis 460
DB 1552 GCAGAGGCTCAGAAACAGACTGTGGAAAGCAGATTAATATCCCTTTCCAGACAT 1611
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAsp 480
DB 1612 TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAAGTTAG 1671
QY 481 IleThrSerAspMetAla 486
DB 1672 ATCAAGTGTATATGGCA 1689
```

RESULT 12

AAS00660

ID AAS00660 standard; cDNA; 3594 BP.

XX AC

AAS00660;

DT 07-SEP-2001 (first entry)

XX

Human TANGO 229 cDNA.

XX

Human; TANGO 229; T cell; heart; liver; pancreas; placenta; brain; lung;

KW skeletal muscle; kidney; spleen; lymph node; peripheral blood leukocyte;

KW bone marrow; thymus tissue; abnormal blood coagulation; asthma; cancer;

KW anaphylaxis; hepatitis; multiple sclerosis; coronary artery disease; se;

KW malaria; atopic dermatitis; amyotrophic lateral sclerosis; meningitis;

KW attention deficit disorder; Crohn's disease; gastroenteritis; goitre;

KW hypoglycaemia; diabetes mellitus; endometriosis; pulmonary embolism;

muscular dystrophy; immuno-competence; vertebrate; blood; serum.
Homo sapiens.

Key Location/Qualifiers
CDS 72..2219
/*tag= a
/*product= "Human TANGO 229"
FT 72..173
/*tag= b
FT 174..2216
/*tag= c
/*product= "Mature human TANGO 229"

WO200129088-A1.

26-APR-2001.

23-JUN-2000; 2000WO-US017386.

19-OCT-1999; 99US-00420707.

(MILL-) MILLENNIUM PHARM INC.

Mackay CR, Myers PS, Kirst SJ, Fraser CC, Leiby KR;

WPI: 2001-308477/32.

P-PSDB; AAU00670.

New isolated nucleic acid molecule for diagnosis, prevention, and therapy of human and other animal disorder, or as modulating agent for regulating cellular processes.

Claim 1; Fig 1; 263pp; English.

The sequence represents a cDNA which encodes human TANGO 229 polypeptide. This protein and similar others exhibit the ability to affect growth, proliferation, survival, differentiation, activity, morphology, or movement/migration of, e.g. T cells and cells of the heart, liver, pancreas, placenta, brain, lung, skeletal muscle, kidney, spleen, lymph node, peripheral blood leukocyte, bone marrow or thymus tissue. They can be used as modulating agents for regulating cellular processes, thus, the proteins and their associated nucleic acids can be used to prognosticate, prevent, diagnose, or treat disorders associated with physiological processes. These disorders include abnormal blood coagulation, asthma, anaphylaxis, hepatitis, multiple sclerosis, cancer, coronary artery disease, malaria, atopic dermatitis, amyotrophic lateral sclerosis, meningitis, attention deficit disorder, Crohn's disease, gastroenteritis, goitre, hypoglycaemia, diabetes mellitus, endometriosis, pulmonary embolism and muscular dystrophy. Antibodies to disorders such as these can be made by providing a polypeptide of the invention to an immuno-competent vertebrate and harvesting blood or serum from the vertebrate.

SQ Sequence 3594 BP; 958 A; 810 C; 921 G; 905 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4,848-225	Length:	3594
Score:	2551.00	Matches:	486
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.77%	Indels:	0
DB:	4	Gaps:	0

US-10-813-588-2 (1-487) x AAS00660 (1-3594)

QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20

DB 228 ATGACATCTAAGAATTATCCCGGACCTACCCCAATCACACTGTTTGGAAAAGCAATT 287

QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40

DB 288 ACAGTACCAAGGGGAAAGAACTGATCTCTAGGTTGGGAGATTGGATATCAATCCAG 347

```
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
DB 348 ACCTGTGCTCTGACTATCTCTCTTACCAGCTCTTCAGATCAATATGTCATACTGT 407
QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
DB 408 GGAAGTATGACTGTTCCCAAGAACTCTTGTTGAACACAAAGTGAAGTAAACCGTCCGCTTT 467
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 468 GAGAGTGGATCCACATTTCTGGCCGGGTTTTTGTGCTGACCTATCGGAGCAGCGACCAT 527
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
DB 528 CCAGATTTAATACATGTTTGGAAACGAGCTAGCCATTATTGGAAGACAGATACAGAAA 587
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 588 TTCGCCCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGAAGA 647
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
DB 648 TATAGAGATACCTCTTTATTGTCCAAAGCTGCCATCCATGCAGCAATAATTGCTGATGA 707
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
DB 708 CTAGGTGGCCAGATCATGTGCTTTCAGCGCAAGGGATCAGTCGATATGAAGGGATTCTG 767
QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB 768 GCCAATGGTGTTCTTTTCGAGGGATGGTTCCTGTGCAGCAAGGATTTCTGTACTCTC 827
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSer 220
DB 828 AATGGTTGCAGCAGATCTTGTAGTTTGAACCTGACGGGCAATATCAGAGCTTCTCTCTCA 887
QY 221 TrpGlnSerValAsnGlnSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 888 TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTTCACTGGTCTCTGGCCAAAGCCGACTT 947
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 948 CAGGACCAAGGCCCATCATGGGCTTCGGGCCACAGTAGCAACCAACCAACCAACGAGAG 1007
QY 261 TrpLeuGluIleAspLeuGlyGluLysLysLysIleThrGlyIleArgThrThrGlySer 280
DB 1008 TGGCTGGAGATCGATTTGGGGGAGAAAAAATAACAGAAATTAGGACCAACAGATCT 1067
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
DB 1068 ACACAGTCGAACTTCAACTTTTATGTTAAGAGTTTTGTGATGAACCTTCAAAAAACAATAAT 1127
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn 320
DB 1128 TCTAAGTGGAGACCTATAAAGGAATTTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1187
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProPheValAlaArgTyrVal 340
DB 1188 TCTAAGTGGAGACCTATAAAGGAATTTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1247
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
DB 1248 CGGGTTTCCCGCCAGACATGCGCCAGAGATAGCTTTGAAGGTGGAGCTCATTTGGTTC 1307
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
DB 1308 CAGATTACAGAGTAATGATTCTTCTGTTGGCGCAAGACAGTCAAGTCAAGCAGATGTT 1367
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
DB 1368 TCAACTAAGAAAGAAGATGAGCAATCACAAGGCCCATCCCTCGGAAGAAACATCCACA 1427
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValPheAla 420
```

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DB 1428 GGAATAAACATTACAAACGGTGCTATTCCATTGGTGCTCTTGTGTCTGTGTTGCT 1487
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysGlySerProTyrGlySer 440
DB 1488 GGAATGGGGATCTTTTGCAGCCTTTAGAAAGAAAGAAAGAAAGGAGTCCGTATGGATCA 1547
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrPropheAlaArgHisGln 460
DB 1548 GCAGAGGCTCAGAAAACAGACTGTTTGAAGCAGCATTAATATATCCCTTTGCCACAGATCAG 1607
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
DB 1608 TCAGCTGAGTTTACCATCAGCTATGATTAATGAAGAGGAGATGACACAAAAGTTAGATCTC 1667
QY 481 IleThrSerAspMetAla 486
DB 1668 ATCACACGTGATATGGCA 1685

RESULT 13
ACD66717
ID ACD66717 standard; cDNA; 3594 BP.
XX
AC ACD66717;
XX
DT 17-SEP-2003 (first entry)
XX
DE Secreted polypeptide-related cDNA #9.
XX
KW Human; gene; ss; TANGO; INTERCEPT; secreted polypeptide; immune disorder;
KW hormonal disorder; proliferative disorder; cancer; thyroid disorder;
KW diabetes; multiple sclerosis; lupus; neurological disorder; anaemia;
KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
KW myocardial infarction; congestive heart disease; blood platelet disorder;
KW thrombocytopenia; blood vessel; atherosclerosis; vasculitis.
XX
OS Homo sapiens.
XX
PN US2003022279-A1.
XX
PD 30-JAN-2003.
XX
PP 12-JAN-2001; 2001US-00759130.
XX
PR 14-JUN-1999; 99US-00333159.
PR 29-JUN-1999; 99US-00342364.
PR 10-SEP-1999; 99US-00393996.
PR 19-OCT-1999; 99US-00420707.
PR 07-JAN-2000; 2000US-00479249.
PR 27-APR-2000; 2000US-00559497.
PR 24-MAY-2000; 2000US-00578063.
PR 16-JUN-2000; 2000US-00596194.
PR 23-JUN-2000; 2000US-00602871.
PR 30-JUN-2000; 2000US-00608452.
XX
(PAS//) FRASER C C.
(PARN//) BARNES T M.
(PHAR//) SHARP J D.
(KIRS//) KIRST S J.
(MYER//) MYERS P S.
(LEIB//) LEIBY K R.
(HOLT//) HOLTZMAN D A.
(MCCA//) MCCARTHY S A.
(WRIG//) WRIGHTON N.
(MACK//) MACKAY C R.
(GOOD//) GOODEARL A D J.
XX
Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KB;
PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;
DR WPI; 2003-456290/43.
DR P-PSDB; AB032527.
XX
```

PT New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,
PT TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or
PT treating disorders such as cancer, diabetes or atherosclerosis, and in
PT forensic biology.

XX Claim 2; Fig 10A-10P; 482pp; English.

CC The invention relates to secreted polypeptide-related proteins and
CC nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The
CC nucleic acids, proteins and antibodies specific to the proteins are
CC useful in screening assays, predictive medicine (e.g. diagnostic assays,
CC prognostic assays, monitoring clinical trials and pharmacogenetics) and
CC prophylactic and therapeutic methods. The sequences are used in
CC diagnosing, preventing or treating proliferative disorders (e.g.
CC cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune
CC disorders (e.g. multiple sclerosis or lupus), neurological disorders
CC (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular
CC disorders (e.g. myocardial infarction or congestive heart disease), blood
CC platelet disorders (e.g. thrombocytopenia or anaemia) and disorders
CC involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic
CC acids may also be used in chromosome mapping, tissue typing and forensic
CC biology, and as surrogate markers. This sequence represents a secreted
CC polypeptide-related cDNA of the invention. Note: The sequence data for
CC this patent was obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html

XX Sequence 3594 BP; 958 A; 810 C; 921 G; 905 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4,84e-225 Length: 3594
Score: 2551.00 Matches: 486
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 8 Gaps: 0

US-10-813-588-2 (1-487) x ACD66717 (1-3594)

QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
DB 228 ATGACATCTAAGATTATCCGGGACCTACCCCAATCACACTGTTTGGGAAAGACAAAT 287
QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
DB 288 ACAGTACCAAGGGGAAAGACGATTCTGAGGTGGAGATTGGATATCGAATCCAG 347
QY 41 ThrCysAlaSerAspTyrIleuLeuPheThrSerSerSerAspClnTyrGlyProTyrCys 60
DB 348 ACCTGTGCTCTGACTATCTCTTCCACGAGCTCTTCAGATCAATATGTCATCTGT 407
QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
DB 408 GGNAGTATGACTGTTCCCAAGNACTCTTGTGTAACAGAGTGAAGTAACCGTCCGCTTT 467
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
DB 468 GAGAGTGGATCCACATTTCTGGCCGGGGTTTTTGTGCTACCTATCCGAGCAGCGACCAT 527
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrIleuLysThrGluTyrSerLys 120
DB 528 CCAGATTTTAAATACATGTTTGGAAACGAGTAGCCATTATTGGAAGACAGAAATACAGCAA 587
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
DB 588 TTCTGCCAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGATATGTTAGTGA 647
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
DB 648 TATAGATACCTCTTTATTTGCAAGCTGCCATCCATGCAGGAATAATTGCTGATGA 707
QY 161 LeuGlyGlyClnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
DB 708 CTAGTGGCCAGATCATGTGTTTCAGCGCAAGGGGATCAGTCGATATGAAGGGATTCTG 767

QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
DB 768 GCCAATGGTGTCTTTTCGAGGGATGGTTCCTGTGCAGACAGAGATTCTGTGTACTCTC 827
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyClnIleArgAlaSerSerSer 220
DB 828 AATGGTTGCAGCAGATCCTTGAACCTGACGGGCAATATCAGAGCTTCTTCTCTCA 887
QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
DB 888 TGGCAGTCCGTCAATGAGAGTGGAGACCAAGTTCACTGGTCTCTCGCCCAAGCCGACTT 947
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 948 CAGGACCAAGGCCCATCATGGCTTCGGGGGACAGTAGACACCAACCAACCAACGAGAG 1007
QY 261 TrpLeuGluIleAspLeuGlyGluLysLysLysIleThrGlyIleArgThrThrGlySer 280
DB 1008 TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAATAACAGGAATTAGGACCAACAGGATCT 1067
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
DB 1068 ACACAGTCAACTTCAACTTTTATGTAAAGAGTTTGTGATGAACCTTCAAAAAACAATAAT 1127
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
DB 1128 TCTAAGTGAAGACCTATTAAGGAATTGTGAATATGAAGAAAGGTGTTTCAGGGTAAAC 1187
QY 321 SerAsnPheAspProValGlnAsnAsnPheIleProProIleValAlaIleArgTyrVal 340
DB 1188 TCTAATCTTTCGGGACCCAGTCGAAAAACAATTTTCATCCCTCCCATCGTGGCCAGATATGTG 1247
QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
DB 1248 CCGGTTGTCTCCCCAGACATGGCCACAGAGGATAGCCTTGAAGGTGGAGCTCATTTGGTTGC 1307
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
DB 1308 CAGATTACACAGGTAATGATTCATTTGGTGTGGCGCAGACAAAGTCANAGCAGCTGTT 1367
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
DB 1368 TCAACTAAGAAAGAGATGAGCAATCAACAAGGCCCATCCCTCCGGAAGAAACATCCACA 1427
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValIleValPheAla 420
DB 1428 GGAATAAAACATTACAAACGGTGGCTATTTCATTTGGTGTCTCTTGTCTGCTGTGTGCT 1487
QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysGlySerProTyrGlySer 440
DB 1488 GGAATGGGATCTTTTCAGCCCTTTAGAAAGAGAGAGAGAGAGAGAGTCCGTATGATCA 1547
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
DB 1548 GCAGAGGCTCAGAAACACAGCTGTTGGAAGCAGATTAATAATATCCCTTTGCCAGACATCAG 1607
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
DB 1608 TCAGCTGAGTTTACCATCAGCTATGATAATGAAGAGAGATGATGACACAAAGTTAGATCTC 1667
QY 481 IleThrSerAspMetAla 486
DB 1668 ATCACAAGTGATATGGCA 1685
RESULT 14
ADQ10134
ID ADQ10134 standard; cDNA; 3594 BP.
XX
AC ADQ10134;
XX
DT 09-SEP-2004 (first entry)
XX

DE Human polynucleotide #10.

XX Human; gene; ss; cancer; obesity; gastritis; diarrhoea; haemorrhoid;
 KW asthma; anaemia; graft-versus-host reaction; allergic reaction;
 KW cystic fibrosis; hypogonadism; cardiovascular disorder; arthritis;
 KW osteoarthritis; arteriosclerosis; hypertension; bacterial infection;
 KW psoriasis; diabetes mellitus; hepatitis; Alzheimer's disease;
 KW Huntington's disease; Parkinson's disease; AIDS; tuberculosis;
 KW viral infection; malaria; goiter; infertility; endometriosis;
 KW muscular disorder.

XX Homo sapiens.

OS US2004121396-A1.

PN 24-JUN-2004.

XX 19-DEC-2003; 2003US-00741790.

XX 14-JUN-1999; 99US-00333159.

PR 29-JUN-1999; 99US-00342364.

PR 10-SEP-1999; 99US-00393996.

PR 19-OCT-1999; 99US-00420707.

PR 07-JAN-2000; 2000US-00479249.

PR 27-APR-2000; 2000US-00559497.

PR 24-MAY-2000; 2000US-00578063.

PR 16-JUN-2000; 2000US-00596194.

PR 23-JUN-2000; 2000US-00602871.

PR 30-JUN-2000; 2000US-00608452.

PR 12-JAN-2001; 2001US-00759130.

XX (MILL-) MILLENNIUM PHARM INC.

XX Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;
 PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADU;
 XX WPI; 2004-479675/45.

XX New TANGO, INTERCEPT, and MANGO, useful in diagnosing, preventing, and
 PT treating cancer, constipation, hemorrhoids, cystic fibrosis,
 PT hypogonadism, psoriasis, hepatitis, Alzheimer's disease, AIDS,
 PT tuberculosis, malaria, goiter, infertility.

XX Claim 2; SEQ ID NO 71; 483pp; English.

XX The invention relates to human polynucleotides and the polypeptides they
 CC encode. The invention also relates to a host cell containing a
 CC polynucleotide of the invention, an antibody which selectively binds with
 CC a polypeptide of the invention, a method of detecting the presence of a
 CC polypeptide in a sample, a method of identifying a compound which binds
 CC with a polypeptide, and a method of modulating the activity of a
 CC polypeptide. The polynucleotides, polypeptides and compositions are
 CC useful for diagnosing, preventing and/or treating cancer, obesity,
 CC gastritis, diarrhoea, haemorrhoids, asthma, anaemia, graft-versus-host
 CC reactions, allergic reactions, cystic fibrosis, hypogonadism,
 CC cardiovascular disorders, arthritis, osteoarthritis, arteriosclerosis,
 CC hypertension, bacterial infections, psoriasis, diabetes mellitus,
 CC hepatitis, Alzheimer's disease, Huntington's disease, Parkinson's
 CC disease, AIDS, tuberculosis, viral infections, malaria, goiter,
 CC infertility, endometriosis, wounds and muscular disorders. This sequence
 CC represents a human polynucleotide of the invention. Note: The sequence
 CC data for this patent did not form part of the printed specification but
 CC was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html.

XX Sequence 3594 BP; 958 A; 810 C; 921 G; 905 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4.84e-225 Length: 3594
 Score: 2551.00 Matches: 486
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.77% Indels: 0

DB: 12 Gaps: 0

US-10-813-588-2 (1-487) x ADQ10134 (1-3594)

QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
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 DB 228 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACCACATGTTTGGCAAGACAAT 287
 |||||
 QY 21 ThrValProLysGlyLysArgLeuLeuLeuArgLeuGlyAspLeuAspIleGluSerGln 40
 |||||
 DB 288 ACAGTACCAGGCGGAAAGAGCTGATTCGAGGTTGGGAGATTTGGATATCGAATCCAG 347
 |||||
 QY 41 ThrCysAlaSerAspTyrIleuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
 |||||
 DB 348 ACCTGTGCTTCTGACTATCTCTCTCCACAGCTCTTCAGATCAATATGTCATCTACTGT 407
 |||||
 QY 61 GlySerMetThrValProLysGluLeuLeuLeuLeuLeuLeuLeuValThrValArgPhe 80
 |||||
 DB 408 GGAAGTATGACTGTTCCCAAGAACTCTTGTGACACAAAGTGAAGTAACCGTCCGCTTT 467
 |||||
 QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
 |||||
 DB 468 GAGAGTGGATCCACATTTCTGCGGGGTTTTTCTGCTGACCTATCGCAGCAGCAGCAT 527
 |||||
 QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrIleuLysThrGluTyrSerLys 120
 |||||
 DB 528 CCAGATTTAATAACATGTTTGAACGAGCTAGCCATATTTTGAAGACAGAAATACAGCAA 587
 |||||
 QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
 |||||
 DB 588 TTCTGCCAGCTGGTTGTAGACAGCTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 647
 |||||
 QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleLeuAlaAspGlu 160
 |||||
 DB 648 TATAGAGATACCTCTTTATTTGTGAAAGCTGCCATCCATGCAGGAATAATTTGCTGATGA 707
 |||||
 QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
 |||||
 DB 708 CTAGGTGGCCAGATCATGTGCTTCAGCCGCAAGGATCAGTCGATATGAAGGATTCGT 767
 |||||
 QY 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
 |||||
 DB 768 GCCAATGGTGTCTTTCGAGGAGTGGTTCCTGTGCAGACAGCATTTCTGTTTACTCC 827
 |||||
 QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSer 220
 |||||
 DB 828 AATGTTGCAGCAGATCTCTGAGTTTGAACCTGCAGCGGCAATCAGAGCTTCTCTCTCA 887
 |||||
 QY 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
 |||||
 DB 888 TGGCAGTCCGTCAATGAGAGTGAGACCAAGTTTCATCTGGTCTCTCGCCCAAGCCGACTT 947
 |||||
 QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
 |||||
 DB 948 CAGGACCAAGGCCCATCTGCGGCTTCGGCGCAGTAGCAACCAACCAACCCAGAGAG 1007
 |||||
 QY 261 TrpLeuGluIleAspLeuGlyLysLysLysIleThrGlyIleArgThrThrGlySer 280
 |||||
 DB 1008 TGGCTCGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAAGATCT 1067
 |||||
 QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
 |||||
 DB 1068 ACACGTGCAACTTCAACTTTTATGTAAAGAGTTTGTGTATGAACTTCAAAAACAATAAT 1127
 |||||
 QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
 |||||
 DB 1128 TCTAAGTGGAGACCTATAAGGAATTTGTAATAATGAAGAAAAGGTGTTTCAGGGTAAC 1187
 |||||
 QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
 |||||
 DB 1188 TCTAACTTTTCGGGACCCAGTCGCAAAACAATTTTCATCTCCCTCCCATCGTGGCCAGATATGT 1247
 |||||
 QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360

Db 1248 CGGGTGTGCCCCCAGACATGGCCACGAGGATAGCTTGAAGTGCGAGCTCATTTGGTTGC 1307
Qy 361 GlnIleThrGlnGlyAsnSerLeuValTTPArgLysThrSerGlnSerThrSerVal 380
Db 1308 CAGATTACCAAGGTAAATGATTCATTTGGTGTGGCGCAAGCAAGTCAAGACCAAGTGT 1367
Qy 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
Db 1368 TCAACTAAGAAAGATGAGCAATACACAGGCCCATCCCTCGGAAGAACATCCACA 1427
Qy 401 GlyIleAsnIleThrThrValIleAlaIleProLeuValLeuValValLeuValPheAla 420
Db 1428 GGAATTAACATTAACAACGGTGGTATTCATTCAGTGGTCTCTTGTCTGGTGTGTGCT 1487
Qy 421 GlyMetGlyIlePheAlaPheArgLysLysLysLysLysGlySerProTyrGlySer 440
Db 1488 GGNATGGGATCTTTTCAGCCCTTTAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1547
Qy 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
Db 1548 GCAGAGGCTCAGAAACAGACTGTTGGAAGCAGATTAAATATCCCTTTCAGACATCAG 1607
Qy 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
Db 1608 TCAGCTGAGTTTACCATCAGCTATGATGATGATGAGAGGAGATGACACAAAGATTAGATCTC 1667
Qy 481 IleThrSerAspMetAla 486
Db 1668 ATCACAAAGTGATATGGCA 1685

RESULT 15

ADL62155

ID ADL62155 standard; DNA; 3676 BP.

XX AC ADL62155;

XX DT 20-MAY-2004 (first entry)

XX DE Human ovarian cancer DNA marker #20367.

XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX OS Homo sapiens.

XX PN WO200170979-A2.

XX PD 27-SEP-2001.

XX PF 21-MAR-2001; 2001WO-US009126.

XX PR 21-MAR-2000; 2000US-0191031P.

XX PR 25-MAY-2000; 2000US-0207124P.

XX PR 15-JUN-2000; 2000US-0211940P.

XX PR 07-JUL-2000; 2000US-0216820P.

XX PR 25-JUL-2000; 2000US-0220661P.

XX PR 21-DEC-2000; 2000US-0257672P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Lee J, Lillie J;

XX DR WPI; 2001-611502/70.

XX PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.

XX PS Disclosure; SEQ ID NO 20367; 106pp; English.

XX CC The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides

CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of the
CC patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 3676 BP; 967 A; 841 C; 953 G; 914 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 4.99e-225 Length: 3676
Score: 2551.00 Matches: 486
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 5 Gaps: 0

US-10-813-588-2 (1-487) x ADL62155 (1-3676)

Qy 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGlyLysThrIle 20
Db 294 ATGACATCTAAGATATATCCCGGACCTACCCCAATCACACTGTTTGGAAAGACAAT 353
Qy 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAspLeuAspIleGluSerGln 40
Db 354 ACAGTACCAGGGGAAAGAAAGACTGATTCTGAGTTGGGAGATTTCGATATCCGATCCAG 413
Qy 41 ThrCysAlaSerAspTyrIleLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
Db 414 ACCTGTGCTTCGACTATCTTCTCTCACAGCTCTTCAGATCAATATGTCCTACTCTG 473
Qy 61 GlySerMetThrValProLysGluLeuLeuAsnThrSerGluValThrValArgPhe 80
Db 474 GGAAGTATGACTGTTCCCAAGAACTCTGTGTGAACACAAAGTGAAGTACCGTCCCTTT 533
Qy 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
Db 534 GAGAGTGGATCCACATTTCTGGCCGGGGTTTTTGTGCTGACCTATCGGAGCAGCCAT 593
Qy 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
Db 594 CCAGATTTAATAACATGTTTGGACGAGCTAGCCATTATTTGAGACACAGAAATACAGCAA 653
Qy 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
Db 654 TTCTCCCGCAGCTGGTGTAGAGACCTAGCAGAGACATTTCTGGGAATATGATATGGA 713
Qy 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleAlaAspGlu 160

Db 714 TATAGAGATACCTCTTTATTGTGCAAAAGCTGCATCCATGCAGGAATAATTGCTGATGAA 773
Qy LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
Db 774 CTAGGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATGAAGGATTCG 833
Qy 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
Db 834 GCCAATGGTGTCTTTTCGAGGGATGGTTCCTGTCAGACAAGCGATTTCTGTTTACCTCC 893
Qy 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
Db 894 AATGGTTGCAGCAGATCCTTGAAGTTTGAACCTGACGGGCAAAATCAGAGCTTCTTCTCA 953
Qy 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
Db 954 TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTCACTGGTCTCTGCGCCAGCCGACCTT 1013
Qy 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
Db 1014 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACCAACCAACCCAGAGAG 1073
Qy 261 TrpLeuGluIleAspLeuGlyGlyLysLysLysIleThrGlyIleArgThrThrGlySer 280
Db 1074 TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAATTAACAGAAATTAGGACCACAGGATCT 1133
Qy 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsnAsn 300
Db 1134 ACACAGTCGAACCTCAACTTTTATGTTAAGAGTTTGTGATGAACCTCAAAAACAATAAT 1193
Qy 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
Db 1194 TCTAAGTGAAGACCTATAAAGGAATTTGTAATAATGAAGAAAAGGTGTTTCAGGGTAAC 1253
Qy 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
Db 1254 TCTAACTTTTCGGGACCCAGTGCAGCAAAACAATTTTCATCCCTCCATCGTGGCCAGATATGT 1313
Qy 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
Db 1314 CGGGTTGTCCCCAGACATGGCACCGACAGAGATAGCCTTGAAGGTGGAGCTCATTTGGTTGC 1373
Qy 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
Db 1374 CAGATTACACAAGGTATGATTTCATTTGGTGTGGCGCAAGACAAGTCAAAGCACCAGTGT 1433
Qy 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
Db 1434 TCAACTAAGAAAGAAGATGAGACANTCACAGGCCCATCCCTCGGAAGAAACATCCACA 1493
Qy 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValLeuValPheAla 420
Db 1494 GGAATAAACATTACAACGGTGGCTATTCCATTGGTGTCTCTTGTCTGGTGGTTTGTCT 1553
Qy 421 GlyMetGlyIlePheAlaIlePheArgLysLysLysLysGlySerProTyrGlySer 440
Db 1554 GGAATGGGATCTTTGCGAGCTTTAGAAAGAAAGAAAGAAAGTCCGATATGGATCA 1613
Qy 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
Db 1614 GCAGAGGCTCAGAAAAACAGACTGTTGAAGCAGATTAAATATCCCTTTGCCAGACATCAG 1673
Qy 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
Db 1674 TCAGTCAGTTTACCATCAGCTATGATATATGAGAAGGAGATGACACAAAAGTTAGATCTC 1733
Qy 481 IleThrSerAspMetAla 486
Db 1734 ATCAAGTGATATGGCA 1751

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2006, 19:22:33 ; Search time 6098 Seconds

(without alignments)
4539.646 Million cell updates/sec

Title: US-10-813-588-2

Perfect score: 2557

Sequence: 1 MTSKNYPGTYPNHTVCEKTI.....YDNEKEMTKQLDITSDMAG 487

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

- Listing first 45 summaries

Command line parameters:

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-DOCLIGN=200 -THR SCORE=pcp -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10813588 @CGN 1.1 7415 @runat_12012006_171131_15391 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

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- 3: gb.env.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pr.*
- 9: gb.ro.*
- 10: gb.sts.*
- 11: gb.sy.*
- 12: gb.un.*
- 13: gb.vi.*
- 14: gb.htg.*
- 15: gb.pl.*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2557	100.0	1464	6 AR542471	Sequence
2	2557	100.0	1464	6 AX118816	Sequence
3	2557	100.0	1620	6 AR542473	Sequence

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

4	2557	100.0	1620	6	AX118820	Sequence
5	2557	100.0	1761	6	AR542472	Sequence
6	2557	100.0	1761	6	AX118818	Sequence
7	2557	100.0	1768	6	AR542474	Sequence
8	2557	100.0	1768	6	AX118822	Sequence
9	2557	100.0	2010	6	CQ870614	Sequence
10	2557	100.0	2010	6	CQ870615	Sequence
11	2557	100.0	2010	8	BC035671	Homo sapi
12	2551	99.8	2888	6	AX704743	Sequence
13	2551	99.8	3676	6	CQ413296	Sequence
14	2512.5	98.3	2547	6	AX833875	Sequence
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16	1415	55.3	2873	5	BC074689	Xenopus t
17	1146.5	44.8	1871	6	BD269864	The poly
18	1146.5	44.8	1871	6	BD269864	Sequence
19	1146.5	44.8	1871	6	AR584212	Sequence
20	1003	39.2	2473	6	CS034882	Sequence
21	1003	39.2	2473	6	CS043834	Sequence
22	1003	39.2	2473	6	AX835251	Sequence
23	1003	39.2	2473	8	AK098194	Homo sapi
24	892.5	34.9	2846	9	BC026771	Mus muscu
25	874	34.2	489	6	CQ718728	Sequence
26	867.5	33.9	2310	6	AR669813	Sequence
27	867.5	33.9	2310	6	AR669814	Sequence
28	867.5	33.9	2339	9	AF387549	Rattus no
29	861.5	33.7	4856	9	BC066097	Mus muscu
30	860.5	33.7	2190	6	AX615195	Sequence
31	860.5	33.7	2280	6	AX615194	Sequence
32	860.5	33.7	2328	6	AR669809	Sequence
33	860.5	33.7	2328	6	AR669810	Sequence
34	860.5	33.7	2939	8	AF387547	Homo sapi
35	860.5	33.7	6093	8	AB073146	Homo sapi
36	856.5	33.5	2310	6	AR669811	Sequence
37	856.5	33.5	2310	6	AR669812	Sequence
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39	853.5	33.4	3858	8	BC029658	Homo sapi
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41	837.5	32.8	2020	6	AX714177	Sequence
42	837.5	32.8	2020	8	AK056350	Homo sapi
43	791.5	31.0	2046	6	BD224188	Factor VI
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ALIGNMENTS

RESULT 1	AR542471	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
LOCUS	AR542471	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
DEFINITION	AR542471	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
ACCESSION	AR542471	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
VERSION	AR542471.1	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
KEYWORDS	AR542471.1	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
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ORGANISM	Unknown.	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
REFERENCE	1 (bases 1 to 1464)	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
AUTHORS	Doncho G., Turner, C.A. Jr., Nehls, M.C., Friedrich, G., Zambrowicz, B. and Sands, A.T.	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
TITLE	Human proteins and polynucleotides encoding the same	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
JOURNAL	Patent: US 6743907-A 1 01-JUN-2004;	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
FEATURES	Lexicon Genetics Incorporated; The Woodlands, TX	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
source	Location/Qualifiers	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
ORIGIN	1..1464	Sequence	1	from patent US 6743907.	1464 bp	DNA	linear	PAT 08-OCT-2004
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QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
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QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
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QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
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QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
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QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
Db 721 CAGGACCAAGGCCCATCATGGGCTTCGGCGCAGTAGCAACAACCAACCAACAGAGAG 780
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Db 841 ACACAGTGGACTTCACTTTTATGTTAAGATTTTGTGATGAATTTCAAAACCAATAT 900
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGlyLysValPheGlnGlyAsn 320
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QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
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QY 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysLysLysLysLys 440
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RESULT 3
AR542473
LOCUS
DEFINITION Sequence 5 from patent US 6743907.
ACCESSION AR542473
VERSION AR542473.1 GI:53934939
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1620)
AUTHORS Donoho,G., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B. and Sands,A.T.
TITLE Human proteins and polynucleotides encoding the same
JOURNAL Patent: US 6743907-A 5 01-JUN-2004;
Lexicon Genetics Incorporated; The Woodlands, TX
FEATURES
source
1..1620
/organism="unknown"
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ORIGIN

Alignment Scores:
Pred. No.: 3 92e-206 Length: 1620
Score: 2557.00 Matches: 487
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-813-588-2 (1-487) x AR542473 (1-1620)

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QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerAspGlnTyrGlyProTyrCys 60
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Db 337 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTAACACAAAGTGAAGTAAACCGTCGCTTT 396
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
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QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
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QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
DB 877 CAGGACCAAGGCCCATCATGGCTTCGGCGCAGACAGTAGCAACCAACCAACCCAGGAG 936
QY 261 TrpLeuGluIleAspLeuGlyGluLysLysLysLysLysLysLysLysLysLysLys 280
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LOCUS
DEFINITION Sequence 3 from patent US 6743907.

ACCESSION AR542472
VERSION AR542472.1 GI:53934938
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1761)
AUTHORS Donoho,G., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B.
and Sands,A.T.
TITLE Human proteins and polynucleotides encoding the same
JOURNAL Patent: US 6743907-A 3 01-JUN-2004;
LEXICON Genetics Incorporated; The Woodlands, TX
FEATURES
source
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/organism="unknown"
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ORIGIN
Alignment Scores: 4.38e-206 Length: 1761
Pred. No.: 2557.00 Matches: 487
Score: 2557.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 6
US-10-813-588-2 (1-487) x AR542472 (1-1761)
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QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
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Qy      481  IleThrSerAspMetAlaGly 487
Db      1738  ATCACAAGTGTATGGCAGGT 1758

RESULT 6
AX118818
LOCUS      AX118818
DEFINITION Sequence 3 from Patent WO0129219.
ACCESSION AX118818
VERSION    AX118818.1 GI:14035775
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
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            Homnidae; Homo.
REFERENCE  1
            Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and
            Sands, A.T.
            Human cub-domain-containing protein and gene encoding the same
            Patent: WO 0129219-A 3 26-APR-2001;
            Lexicon Genetics Incorporated (US)

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ORIGIN
Alignment Scores:      4.38e-206      Length:      1761
Pred. No.:            2557.00      Matches:      487
Score:                100.00%      Conservative: 0
Percent Similarity:   100.00%      Mismatches: 0
Best Local Similarity: 100.00%      Indels:      0
Query Match:         100.00%      Gaps:        0
DB:                   6

US-10-813-588-2 (1-487) x AX118818 (1-1761)

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QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
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QY 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
Db 1318 CGGGTTGTCCCCCAGACATGGCCACGAGGATAGCCTTGAAGGTGGAGCTCATTTGGTTGC 1377
QY 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
Db 1378 CAGATTACACAAGGTAATGATTGTTGGTGTGGCGCAAGCAAAAGTCANAGCACCACTGTT 1437
QY 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
Db 1438 TCNACTAAGAAAGAGTGACACATACAGAGCCCATCCCTCGGAAGAAACATCCACA 1497
QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuValValLeuValPheAla 420
Db 1498 GGAATAAACATTACAAACGGTGGCTATTCATTGGTGTCTCTTGTCTCTGGTTTGTCT 1557
QY 421 GlyMetGlyIlePheAlaPheArgLysLysLysLysLysGlySerProTyrGlySer 440
Db 1558 GGAATGGGATCTTTCCAGCCTTTAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1617
QY 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
Db 1618 GCGGAGCTCAGAAACAGACTGTTGGAAGCAGATTAATATCCCTTTGCCAGACATCAG 1677
QY 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
Db 1678 TCAGCTGAGTTTACCATCAGCTATGATGATGATGATGATGATGATGATGATGATGAT 1737
QY 481 IleThrSerAspMetAlaGly 487
Db 1738 ATCAAGAAGTATGGCAGGT 1758

RESULT 7
AR542474
LOCUS AR542474 1768 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 7 from patent US 6743907.
ACCESSION AR542474
VERSION AR542474.1 GI:53934940
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1768)
AUTHORS Donoho, G., Turner, C.A. Jr., Nehls, M.C., Friedrich, G., Zambrowicz, B.
and Sands, A. T.
TITLE Human proteins and polynucleotides encoding the same
JOURNAL Patent: US 6743907-A 7 01-JUN-2004;
FEATURES Lexicon Genetics Incorporated; The Woodlands, TX
source Location/Qualifiers
1..1768
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 4,4e-206 Length: 1768
Score: 2557.00 Matches: 487
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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US-10-813-588-2 (1-487) x AR542474 (1-1768)
QY 1 MetThrSerLysAsnTyrProGlyThrTyrProAsnHisThrValCysGluLysThrIle 20
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QY 21 ThrValProLysGlyLysArgLeuIleLeuAtgLeuGluAspLeuAspIleGluSerGln 40
Db 119 ACATGATACCAAGGGGAAAGACATCTCTGAGGTGGGAGATTGGATATCGAATCCAG 178
QY 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
Db 179 ACTGTGCTTCTGACTATCTTCTTCCACGACTCTTCAGATCAATATGGTCCATAGTGT 238
QY 61 GlySerMetThrValProLysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
Db 239 GGAAGTATGACTGTTTCCCAAGAACTCTTGTGTAACAACAAGTGAAGTAACCGTCCGCTT 298
QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
Db 299 GAGAGTGGATCCACATTTCTGCCCGGGGTTTTTCTGCTACCTATCGGACGACGACCAT 358
QY 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
Db 359 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACAGCAA 418
QY 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
Db 419 TTCTGCCACAGCTGGTGTGTAGACGCTAGCAGGAGACATTTCTGGGAATATGGTAGTGA 478
QY 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
Db 479 TATAGATGATCTCTTTATTTGCAAGCTGCATCCATCCATGCAAGAAATATTTGCTGATGA 538
QY 161 LeuGlyGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
Db 539 CTAGGTGGCCAGATCAGTGTCTTACGCCAAAGGGATCAGTCGATATGAAGGATTTCTG 598
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Db 599 GCCAATGGTGTCTTTTCGAGGGATGGTTCCCTGTGTCAGACACGAGATTTCTGTTTACCTCC 658
QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
Db 659 AATGTTGCAGCAGATCTCTTGTAGTTTGAACCTGACGGCAATTCAGACTTCTTCTCTCA 718
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Db 719 TGGCAGTGGTCAATGAGAGTGGAGACCAAGTTCACTGGTCTCTTGGCCCAAGCCGACTT 778
QY 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
Db 779 CAGGACCAAGGCCCATCATCTGGCTTTCGGGCGACAGTAGCAACAACCAACCCACGAGAG 838
QY 261 TrpLeuGluIleAspLeuGlyLysValLysIleThrGlyIleArgThrThrGlySer 280
Db 839 TGGCTGGAGATCGATTTGGGGGAGAAAGAAATAAACAGGAATTAGGACCAACAGATCT 898
QY 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
Db 899 ACACAGTCGAACCTTCAACCTTTTATGTTAAGAGTGTGTTGATGAACCTTCAAAACAATAAT 958
QY 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
Db 959 TCTAAGTGGAGACCTATAAAGGAAATTTGTAATAATGAAGAAAGGTGTTTTCAGGGTAAC 1018
QY 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProProIleValAlaArgTyrVal 340
Db 1019 TCTAACTTTCGGGACCCAGTGCAGAAACAATTTTCATCTCCCTCCATCTGTCGCCAGATATGTG 1078
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 Db 1139 CAGATTACACAGGTATGATTCATTTGGTGTGGCGCAGACAGTCAAGACCATGTT 1198
 QY 381 SerThrLysLysGluAepGluThrIleThrArgProIleProSerGluGluThrSerThr 400
 Db 1199 TCAACTAAGAAAGAAAGATGAGACATCACAAAGGCCCATCCCTCGGAAGAAACATCCACA 1258
 QY 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValPheAla 420
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 Db 1319 GGAATGGGATCTTTGCAGCTTTAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGATCA 1378
 QY 441 AlaGluAlaGlnLysThrAepCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
 Db 1379 GCGAGGCTCAGAAACACAGACTGTTCGAGCAGATTAAATATATCCCTTTGCGACATCAG 1438
 QY 461 SerAlaGluPheThrIleSerTyrAepAsnGluLysGluMetThrGlnLysLeuAepLeu 480
 Db 1439 TCAGCTGAGTTTACCATCAGCTATGATATGAGAGAGAGATGACACAAAGTTAGATCTC 1498
 QY 481 IleThrSerAepMetAlaGly 487
 Db 1499 ATCACAAGTATATGGCAGT 1519

RESULT 8

AX118822
 LOCUS AX118822
 DEFINITION Sequence 7 from Patent WO0129219.
 ACCESSION AX118822
 VERSION AX118822.1 GI:14035777

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens (human)
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Homo.

REFERENCE

1 Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and
 Sands, A.T.
 Human cub-domain-containing protein and gene encoding the same
 Patent: WO 0129219-A 7 26-APR-2001;
 JOURNAL Lexicon Genetics Incorporated (US)

FEATURES

source
 1..1768
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:
 Pred. No.: 4,46-206 Length: 1768
 Score: 2557.00 Matches: 487
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-813-588-2 (1-487) x AX118822 (1-1768)

QY 1 MetThrSerLysAsnTyrProGlyThrTyrProHisThrValCysGluLysThrIle 20
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 QY 21 ThrValProLysGlyLysArgLeuIleLeuArgLeuGlyAepLeuAepIleGluSerGln 40
 Db 119 ACAGTACCAAGGGGAAAGAAAGACTGATCTCGAGGTTGGAGATTGGATATCGATCCAG 178

QY 41 ThrCysAlaSerAepTyrIleLeuPheThrSerSerSerAepGlnTrrGlyProTyrCys 60
 Db 179 ACCTGTGCTTCTGACTATCTTCTTACCAGCTCTTCAGATCAATATGGTCATCTGT 238
 QY 61 GlySerMetThrValProLysGluLeuLeuLeuAenThrSerGluValThrValArgPhe 80
 Db 239 GGAAGTATGACTGTTTCCCAAGAACTCTTGTGTAACACAAAGTGAAGTAAACCGTCCGCTTT 298
 QY 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAepHis 100
 Db 299 GAGAGTGGATCCACCATTTCTGCGCGGGTTTTTGTGCTGACCTATGCGAGCAGCGACCAT 358
 QY 101 ProAepLeuIleThrCysLeuGluArgAlaSerHisTyrIleLysThrGluTyrSerLys 120
 Db 359 CCAGATTTTAAATACATGTTTGAACAGAGCTAGCCATATTATTGAAGACAGAAATACACAAA 418
 QY 121 PheCysProAlaGlyCysArgAepValAlaGlyAepIleSerGlyAsnMetValAepGly 140
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 QY 141 TyrArgAepThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAepGlu 160
 Db 479 TATAGAGATACCTCTTTATTGTGCAAGCTGCCATCCATGCAGGAATAATTGCTGATGAA 538
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 QY 201 AsnGlyCysSerArgSerLeuSerPheGluProAepGlyGlnIleArgAlaSerSer 220
 Db 659 AATGGTTGCAGCAGATCTTTGAGTTTTGAACCTGCAGCGGCAATATCAGAGCTTCTTCTCA 718
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RESULT 10

LOCUS CQ870615 2010 bp DNA linear PAT 13-SBP-2004
 DEFINITION Sequence 24 from Patent WO2004073657.
 ACCESSION CQ870615

VERSION CQ870615.1 GI:52000126

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE

1 Aziz, N., Gish, K.C., Wilson, K.E. and Zlotnik, A.

AUTHORS Methods of diagnosis of cancer, composition and methods of
 TITLE screening for modulators of cancer

JOURNAL Patent: WO 2004073657-A 24 02-SEP-2004;

PROTEIN DESIGN LABS, INC. (US)

FEATURES

source
 1. 2010
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 5.2e-206 Length: 2010
 Score: 2557.00 Matches: 487
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-813-588-2 (1-487) x CQ870615 (1-2010)

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DB 702 TATAGAGATACCTCTTTATTGTGCAAGCTGCCATCCATCCAGGATAATATGCTGATGAA 761
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 QY 481 IleThrSerAspMetAlaGly 487
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RESULT 11

BC035671

LOCUS

BC035671 2010 bp mRNA linear PRI 25-JUL-2005

DEFINITION Homo sapiens discoidin, CUB and LCCL domain containing 1, mRNA
 (cDNA clone MGC:46341 IMAGE:5730536), complete cds.

ACCESSION BC035671
 VERSION BC035671.1 GI:23274238
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2010)
 AUTHORS Strausberg,K.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altshuler,S.P., Zerborg,B., Buetow,K.H., Schaefer,C.P., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,P., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stappleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalusz,D.B., Schnerch,A., Schein,J.E., Jones,S.J. and Young,A.C., 2001. The Mammalian Gene Collection Program Team
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932

REFERENCE 2 (bases 1 to 2010)
 AUTHORS NIH MGC Project
 TITLE Direct Submission
 JOURNAL Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 CONTACT: MGC help desk
 EMAIL: cgabs-remail.nih.gov
 Tissue Procurement: Invitrogen
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NIHC),
 Gaithersburg, Maryland;
 Web site: <http://www.nih.gov/>
 Contact: nihc.mgc@nih.gov
 Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Young,A., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 79 Row: i Column: 21
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27735142.
 Location/Qualifiers

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ORIGIN
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 US-10-813-588-2 (1-487) x BC035671 (1-2010)

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REFERENCE
AUTHORS Guraajan, R., Hafalia, A.J., Kallick, D.A., Patterson, C., Azimzai, Y.,
Khan, F.A., Xu, Y., Yao, M.G., Yue, H., Au-Young, J., Batra, S.,
Baughn, M.R., Borowsky, E.A., Lo, T.P., Lu, D.A., Lu, Y., Tang, Y.T.,
Yang, J., Zingler, K.A., Deleage, A.M., Gietzen, K., Marcus, G.A.,
Nguyen, D.B., Policky, J.L., Ramkumar, J., Thangavelu, K., Walla, N.K.
and Warren, B.A.
TITLE Human extracellular matrix and cell adhesion polypeptides
JOURNAL Patent: WO 020634-A 47 10-JAN-2002;
INCYTE GENOMICS INC. (US)
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US-10-813-588-2 (1-487) x AX704743 (1-2888)

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SOURCE Homo sapiens
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Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 20367 27-SEP-2001;

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 VERSION AX833875.1 GI:39920010
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Homnidae; Homo.
 REFERENCE 1
 AUTHORS Isegai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,
 Yamamoto, J.I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,
 Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahara, K. and
 Masuho, Y.
 TITLE Full-length cDNA sequences
 JOURNAL Patent: EP 1347046-A 999 24-SEP-2003;
 Research Association for Biotechnology (JP)
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 QY 261 TrpLeuGluIleAspLeuGlyLysLysLysLysLysLysLysLysLysLysLysLys 280
 DB 985 TGGCTGGAGATCGAATTTGGGGGAGAAAAGAAAATACAGAAATTAGGACCAACAGGATCT 1044
 QY 281 ThrGlnSerAsnPheAsnPheTrpValLysSerPheValMetAsnPhelYsAsnAsn 300
 DB 1045 ACACAGTCGAACCTTCAACTTTATGTTAAGAGTTTGTGATGATCTTCAAAAACAATAAT 1104
 QY 301 SerLysTrpLysThrTrpLysGlyIleValAsnAsnGluLysValPheGlnGlyAsn 320
 DB 1105 TCTAAGTGGAAAGACCTATAAAGAAATGTGAATAATGAAGAAAGGTGTTTTCAGGGTAAC 1164

Db 205 ATGACATCTAAGATTATATCCCGGACCTACCCCAATCACACTGTTTGGGAAAGACAAT 264
Qy 21 ThrValProlysGlyLysArgLeuLeuLeuArgLeuGlyAspLeuAspIleGluSerGln 40
Db 265 ACAGTACCAAGGGGAAAGACTGATCTGAGGTGGAGATTGGATATCGAATCCAG 324
Qy 41 ThrCysAlaSerAspTyrLeuLeuPheThrSerSerSerAspGlnTyrGlyProTyrCys 60
Db 325 ACCTGTGCTTCTGACTATCTCTCTCCACGAGCTCTTCAGATCAATATGGTCCATACTGT 384
Qy 61 GlySerMetThrValProlysGluLeuLeuLeuAsnThrSerGluValThrValArgPhe 80
Db 385 GGAAGTATGACTGTCTCCAAAGAACTCTTGTTGAACACAAAGTGAAGTAACCGTCCGCTTT 444
Qy 81 GluSerGlySerHisIleSerGlyArgGlyPheLeuLeuThrTyrAlaSerSerAspHis 100
Db 445 GAGAGTGGATCCCAATCTTGGCCGGGTTTTTGTGACCTATGCGAGCAGGACCAT 504
Qy 101 ProAspLeuIleThrCysLeuGluArgAlaSerHisTyrLeuLysThrGluTyrSerLys 120
Db 505 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA 564
Qy 121 PheCysProAlaGlyCysArgAspValAlaGlyAspIleSerGlyAsnMetValAspGly 140
Db 565 TTCTGCCCGAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGA 624
Qy 141 TyrArgAspThrSerLeuLeuCysLysAlaAlaIleHisAlaGlyIleIleAlaAspGlu 160
Db 625 TATAGAGATACCTCTTTATTTGCAAGCTGCCATCCATGCAGGAATAATGCTGATGAA 684
Qy 161 LeuGlyGlnIleSerValLeuGlnArgLysGlyIleSerArgTyrGluGlyIleLeu 180
Db 685 CTAGGTGGCCAGATCAGTGTGCTTTCAAGCAAAAGGATCAGTCGATATGAAGGGATTCG 744
Qy 181 AlaAsnGlyValLeuSerArgAspGlySerLeuSerAspLysArgPheLeuPheThrSer 200
Db 745 GCCAATGGTGTCTTTTCAGGGATGGTTCCTGTGCAGCAAGCGATTCTGTTCACCTCC 804
Qy 201 AsnGlyCysSerArgSerLeuSerPheGluProAspGlyGlnIleArgAlaSerSerSer 220
Db 805 AATGGTTGCAGCAGATCTCTTGAGTTTTGAACTGACGGCAATTCAGAGCTTCTTCCTCA 864
Qy 221 TrpGlnSerValAsnGluSerGlyAspGlnValHisTrpSerProGlyGlnAlaArgLeu 240
Db 865 TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTCACTGGTCTCCTGGCCAAAGCCCGACTT 924
Qy 241 GlnAspGlnGlyProSerTrpAlaSerGlyAspSerSerAsnAsnHisLysProArgGlu 260
Db 925 CAGGACCAAGCCCATCATGGGCTTCGGGCGACAGTAGCAACAACCAACCAACGAGAG 984
Qy 261 TrpLeuGluIleAspLeuGlyLysLysIleThrGlyIleArgThrThrGlySer 280
Db 985 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGCCACAGGATCT 1044
Qy 281 ThrGlnSerAsnPheAsnPheTyrValLysSerPheValMetAsnPheLysAsnAsn 300
Db 1045 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAAACAATA 1104
Qy 301 SerLysTrpLysThrTyrLysGlyIleValAsnAsnGluGluLysValPheGlnGlyAsn 320
Db 1105 TCTAAGTGGAGACCTATTAAGGAATTTGTGAATATGAGAAAAGGTGTTTCAGGGTAAC 1164
Qy 321 SerAsnPheArgAspProValGlnAsnAsnPheIleProPheIleAlaArgTyrVal 340
Db 1165 TCTAACTTTTGGGACCCAGTCGCAAAAACAATTTCACTCCCTCCATCGTGGCCAGATATGT 1224
Qy 341 ArgValValProGlnThrTrpHisGlnArgIleAlaLeuLysValGluLeuIleGlyCys 360
Db 1225 CGGGTGTGCCCCAGACATGGCACCAGAGGATAGCTTTGAAGGTGGAGCTCATTTGGGTGC 1284
Qy 361 GlnIleThrGlnGlyAsnAspSerLeuValTrpArgLysThrSerGlnSerThrSerVal 380
Db 1285 CAGATTACAAAGGTAATGATTCTATTTGTTGGGCGCAGACAAAGTCAAAAGCACCAGTGT 1344

Qy 381 SerThrLysLysGluAspGluThrIleThrArgProIleProSerGluGluThrSerThr 400
Db 1345 TCAACTTAAGAAAGAGATGAGACAATCACAGGCCCATCCCCCTCGAAGAAACATCCACA 1404
Qy 401 GlyIleAsnIleThrThrValAlaIleProLeuValLeuLeuValValPheAla 420
Db 1405 GGAATAAAACATTACAAACGGTGGCTATTCATTTGGTGCTCTCTGTGTCTCGGTGTTGCT 1464
Qy 421 GlyMetGlyIlePheAlaAlaPheArgLysLysLysLysLysLysLysLysLysLys 440
Db 1465 GGAATGGGATCTTTGCAGCCTTTAG-----AAAAAGAAAGAAAGTCCGTATGGATCA 1520
Qy 441 AlaGluAlaGlnLysThrAspCysTrpLysGlnIleLysTyrProPheAlaArgHisGln 460
Db 1521 GCAGAGGCTCAGAAAAACAGACTGTTGGAAGCAGATTAAATATATCCCTTTGCCAGACATCAG 1580
Qy 461 SerAlaGluPheThrIleSerTyrAspAsnGluLysGluMetThrGlnLysLeuAspLeu 480
Db 1581 TCAGCTGAGTTTACCATCAGCTATGATAATGAGAGGAGATGACACAAAAGTTAGATCTC 1640
Qy 481 IleThrSerAspMetAla 486
Db 1641 ATCACAAGTGATATGGCA 1658

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Job time : 6126 secs

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RESULT 2
US-11-128-061-3655
; Sequence 3655, Application US/11128061
; Publication No. US2006003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Monte, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3655
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-128-061-3655

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	Query Match	5.4%; Score 78.4; DB 7; Length 1400;
	Best Local Similarity	54.1%; Pred. No. 7.8e-15;
	Matches 210; Conservative	0; Mismatches 166; Indels 12; Gaps 2;
Qy	696 CTGGTCTCCTGGCCAAAGCGGACATTCAGGACCAAGGCCCATCATGCGGTCTCGGGCGCACAG	755
Dd		
	1007 CTGGTCTCCTTCAAAGAAGCTCGACTTCACCTCCAAG-----GAGGAGTAATGCCTGGAG	1060
Qy	756 TAGCAACAACCAAAAACACAGAGTAGTGCTGGAGATCGATTTGGGGGGAAGAAAAAGAAAT	815
Dd	1061 ACCTTCAGGTCGAATAATCCAAAGAAGTAGTGCTCAAGTGGACTTCACAGAAGCACAATGAAAGT	1120
Qy	816 AACAGGAATTAGGACCACAGAGATCTACACAGTCGAACTTCCAACTTTATTGTTAAGAGATT	875
Dd	1121 CACAGGAGTAAGTACTCTCAGGAGTAANAATCTCTGTTACCAAGCATGTATGTGAAGGAGTT	1180
Qy	876 TGTGATGAACTTCAA AAAACAATAATTTCTTAAGTGAAGACCTATTAAGGAATTTGTGAATAA	935
Dd	1181 CCTCATCTCCAGCAGTCGAAGATGCCCATCAGTGGACTCTCTTTT-----TTCAAGATGG	1234
Qy	936 TGAAGAAAAGGTGTTTTCAGGAGTAACCTTAACTTTTCGGGACCCAGTCGAAAAACAATTTTCAT	995

	Db	1235	CAAAAGTAAGGTTTTTCAGGGAAATCAAGAATCTCCTTACACCTGTGGTGACTCTCTAGA	1299
	Qy	996	CCCTCCCATCGTGGCCAGATATGTGCGGGTTGTCCCCCAGACATGCCACCAGAGGATAGC	1055
	Db	1295	CCCACCGTTACTGACTCGCTACCTTCGAATTCACCCCAGAGTTGGGTGCACAGATTGC	1354
	Qy	1056	CTTGAAGTGGAGCTCAATTTGGTTGCCAG	1083
	Db	1355	CCTGAGATGGAGGTTCTGGGCTGCGAG	1382
 RESULT 3 US-11-128-061-13				
; Sequence 13, Application US/11128061				
; Publication No. US20060003958A1				
; GENERAL INFORMATION:				
; APPLICANT: Melville, Mark W.				
; APPLICANT: Charlebois, Timothy S.				
; APPLICANT: Mounts, William M.				
; APPLICANT: Hann, Louane E.				
; APPLICANT: Sinacore, Martin S.				
; APPLICANT: Leonard, Mark W.				
; APPLICANT: Brown, Eugene L.				
; APPLICANT: Miller, Christopher P.				
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS				
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION				
; FILE REFERENCE: 01997.027701				
; CURRENT APPLICATION NUMBER: US/11/128,061				
; CURRENT FILING DATE: 2005-05-11				
; PRIOR APPLICATION NUMBER: US 60/570,425				
; PRIOR FILING DATE: 2004-05-11				
; NUMBER OF SEQ ID NOS: 7285				
; SOFTWARE: PatentIn version 3.3				
; SEQ ID NO 13				
; LENGTH: 4374				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
US-11-128-061-13				
 Query Match 5.4%; Score 78.4; DB 7; Length 4374;				
Best Local Similarity 54.1%; Pred. No. 1.7e-14;				
Matches 210; Conservative 0; Mismatches 166; Indels 12; Gaps 2;				
	Qy	696	CTGGTCTCTCTGGCCAACGCCCGACTTCAGGACCAAGGCCCATCATATGGGCTTCGGGCGCACAG	755
	Db	3981	CTGGTCTCTCTCAAAGCTCGACTTCACCTCCAAG-----GAGGAGTAATGCCTGGAG	4034
	Qy	756	TAGCAACAACCAACCAACAGAGTGGCTGGAGATCGAATTTGGGGGAGAAAAGAAAT	815
	Db	4035	ACCTCAGGTGAATAATCCAAAGAGTGGCTGCAAGTGGACTTCCAGAAGACAATGAAGT	4094
	Qy	816	AACAGGAATTAGGACCAACAGATCTACACAGTCGAATCTCAACTTTATGTTAAGAGTTT	875
	Db	4095	CACAGGAGTACTACTCAGGAGGTAAATCTCTGCTTACCAAGCATATGTTGAAGGNTT	4154
	Qy	876	TGTGATGAATCTCAAAAAACAATAATTCTAAGTGGAGAACCTATAAAGGAAATGTGTAATAA	935
	Db	4155	CCTCATCTCCAGCAGTCAGAATGCCATCAGTGGACTCTCTTT-----TTCAGAAATGG	4208
	Qy	936	TGAAGAAAAGTGTTCAGGGTAACTCTAACTTTCCGGACCCAGTGC AAAACAATTTTCAT	995
	Db	4209	CAAAAGTAAGGTTTTTTCAGGGAAAATCAAGACTCCTTTCACACCTGTGGTGAATCTCTTAGA	4268
	Qy	996	CCCTCCCATCGTGGCCAGATATGCGGGTTGTCCCCCAGACATGGCACACAGAGGATAGC	1055
	Db	4269	CCCACCGTACTGACTCGCTACCTTCGAATTCACCCCCAGAGTTGGGTGCCACGATTGC	4328
	Qy	1056	CTTGAAGTGGAGTCATTTGGTTGCCAG	1083
	Db	4329	CCTGAGATGGAGGTTCTTGGGCTGCGAG	4356

RESULT 4

US-10-632-645-14
; Sequence 14, Application US/10632645
; Publication No. US20050276787A1
; GENERAL INFORMATION:
; APPLICANT: Couto, Linda B.
; APPLICANT: Colosi, Peter C.
; TITLE OF INVENTION: Adeno-Associated Vectors for Expression of Factor VIII
; FILE REFERENCE: Avigen-04082
; CURRENT APPLICATION NUMBER: US/10/632,645
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/740,211
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/470,618
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/125,974
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/104,994
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 4999

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-632-645-14

Query Match 5.4%; Score 78.4; DB 6; Length 4999;
Best Local Similarity 54.1%; Pred. No. 1.9e-14;
Matches 210; Conservative 0; Mismatches 166; Indels 12; Gaps 2;
QY 696 CTGGTCTCTGGCCAAAGCCGACTTCAGACCAAGCCCATCATGCGGCTTCGGGCGACAG 755
Db 4396 CTGGTCTCTTCAAAAGCTCGACTTCACCTCCAAGG-----GAGGAGTAATGCTGGAG 4449
QY 756 TAGCAACAACCAACCAAGAGTGGCTGGAGATCGATTTGGGGGAGAAAGAAAT 815
Db 4450 ACCTCAGGTGAATATCCAAAGAGTGGCTGCAAGTGGACTTCCAGAAACATGAAGT 4509
QY 816 AACAGGAATTAGGACCAAGAGTCTACAGATCGAACTTCAACTTTATTTTAAAGATT 875
Db 4510 CACAGGAGTAACCTACTCAGGAGTAAATCTCTGCTTACAGCATGTATGTGAAGATT 4569
QY 876 TGTGTGAATCTCAAAACATATTTCTAAGTGAAGACCTATAAGGAATTTGTGAATA 935
Db 4570 CCTCATCTCCAGCAGTCAAGATGGCCATCAGTGGACTCTCTTTT-----TTCAGAAATGG 4623
QY 936 TGAAGAAAAGGTGTTTTCAGGTAACCTAACTTTGGGACCCAGTGCAGAAACAATTTTCAT 995
Db 4624 CAAAGTAAAGTTTTCAGGGAATCAAGACTCTTACACCTGTGTGTAATCTCTAGA 4683
QY 996 CCTCCCATGTCGCCAGATATGTGGGGTGTGTCCTCCAGACATGCGACCAAGGATAGC 1055
Db 4684 CCACCCGTACTGACTCGCTACCTTCGAATTCACCCCGAGAGTTGGTGCACCAAGATTGC 4743
QY 1056 CTGAGGTGGAGCTCATTTGGTTGGCAG 1083
Db 4744 CTTGAGGTGGAGGTTCTGGGCTGGCAG 4771

RESULT 5

US-10-632-645-13
; Sequence 13, Application US/10632645
; Publication No. US20050276787A1
; GENERAL INFORMATION:
; APPLICANT: Couto, Linda B.
; APPLICANT: Colosi, Peter C.
; TITLE OF INVENTION: Adeno-Associated Vectors for Expression of Factor VIII
; FILE REFERENCE: Avigen-04082

; CURRENT APPLICATION NUMBER: US/10/632,645
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/740,211
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/470,618
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/125,974
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/104,994
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 11933

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-632-645-13

Query Match 5.4%; Score 78.4; DB 6; Length 11933;
Best Local Similarity 54.1%; Pred. No. 3.5e-14;
Matches 210; Conservative 0; Mismatches 166; Indels 12; Gaps 2;
QY 696 CTGGTCTCTGGCCAAAGCCGACTTCAGACCAAGCCCATCATGCGGCTTCGGGCGACAG 755
Db 4371 CTGGTCTCTTCAAAAGCTCGACTTCACCTCCAAGG-----GAGGAGTAATGCTGGAG 4424
QY 756 TAGCAACAACCAACCAAGAGTGGCTGGAGATCGATTTGGGGGAGAAAGAAAT 815
Db 4425 ACCTCAGGTGAATATCCAAAGAGTGGCTGCAAGTGGACTTCCAGAAACATGAAGT 4484
QY 816 ACAGGAATTAGGACCAAGAGTCTACAGATCGAACTTCAACTTTATTTTAAAGATT 875
Db 4485 CACAGGAGTAACCTACTCAGGAGTAAATCTCTGCTTACAGCATGTATGTGAAGATT 4544
QY 876 TGTGTGAATCTCAAAACAATAATTTCTAAGTGAAGACCTATAAGGAATTTGTGAATA 935
Db 4545 CCTCATCTCCAGCAGTCAAGATGGCCATCAGTGGACTCTCTTTT-----TTCAGAAATGG 4598
QY 936 TGAAGAAAAGGTGTTTTCAGGTAACCTTAACTTTTCGGGACCCAGTGCAGAAACAATTTTCAT 995
Db 4599 CAAAGTAAAGTTTTCAGGGAATCAAGACTCTCTTACACCTGTGTGTAATCTCTAGA 4658
QY 996 CCTCCCATGTCGCCAGATATGTGGGGTGTGTCCTCCAGACATGCGACCAAGGATAGC 1055
Db 4659 CCCACCGTTACTGACTCGCTACCTTCGAATTCACCCCGAGAGTTGGTGCACCAAGATTGC 4718
QY 1056 CTTGAGGTGGAGCTCATTTGGTTGGCAG 1083
Db 4719 CTTGAGGTGGAGGTTCTGGGCTGGCAG 4746

RESULT 6

US-11-136-527-989/c
; Sequence 989, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays for Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 989
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-989


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; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3786
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-3786

Query Match          3.6%; Score 52.4; DB 6; Length 201;
Best Local Similarity 58.2%; Pred. No. 6.8e-07;
Matches 92; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 926 TTGTGAATATGAAGAAAGGTGTTTCAGGGTAACCTCTAACTTTCCGGACCCAGTGCAAA 985
DB 10 TTCAAGATGGCAAGTAAGGTTTTTCAGGAAATCAAGACTCTTCACACCTGTGTGA 69

QY 986 ACAATTTTCATCCCTCCCATCGTCCAGATATGTGGGGTTGTCCCCAGACATGGCACC 1045
DB 70 ACTCTAGACCCACCGTTACTGACTCGCTASCTTGAATTCACCCCCAGAGTTGGGTGC 129

QY 1046 AGAGGATAGCTTGAAGGTGAGCTCATTTGGTGGCAG 1083
DB 130 ACCAGATTGCCCTGAGGATGGAGGTTCTGGGCTGCGAG 167

RESULT 13
US-10-995-561-3851
; Sequence 3851, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3851
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-3851

Query Match          3.6%; Score 52.4; DB 6; Length 201;
Best Local Similarity 58.2%; Pred. No. 6.8e-07;
Matches 92; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 926 TTGTGAATATGAAGAAAGGTGTTTCAGGGTAACCTCTAACTTTCCGGACCCAGTGCAAA 985
DB 10 TTCAAGATGGCAAGTAAGGTTTTTCAGGAAATCAAGACTCTTCACACCTGTGTGA 69

QY 986 ACAATTTTCATCCCTCCCATCGTCCAGATATGTGGGGTTGTCCCCAGACATGGCACC 1045
DB 70 ACTCTAGACCCACCGTTACTGACTCGCTASCTTGAATTCACCCCCAGAGTTGGGTGC 129

QY 1046 AGAGGATAGCTTGAAGGTGAGCTCATTTGGTGGCAG 1083
DB 130 ACCAGATTGCCCTGAGGATGGAGGTTCTGGGCTGCGAG 167

RESULT 14
US-10-995-561-3853
; Sequence 3853, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
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; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3853
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-3853

Query Match          3.6%; Score 52.4; DB 6; Length 201;
Best Local Similarity 58.2%; Pred. No. 6.8e-07;
Matches 92; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 926 TTGTGAATATGAAGAAAGGTGTTTCAGGGTAACCTCTAACTTTCCGGACCCAGTGCAAA 985
DB 15 TTCAAGATGGCAAGTAAGGTTTTTCAGGAAATCAAGACTCTTCACACCTGTGTGA 74

QY 986 ACAATTTTCATCCCTCCCATCGTCCAGATATGTGGGGTTGTCCCCAGACATGGCACC 1045
DB 75 ACTCTAGACCCACCGTTACTGACTBGCTACCTTGAATTCACCCCCAGAGTTGGGTGC 134

QY 1046 AGAGGATAGCTTGAAGGTGAGCTCATTTGGTGGCAG 1083
DB 135 ACCAGATTGCCCTGAGGATGGAGGTTCTGGGCTGCGAG 172

RESULT 15
US-10-995-561-3984
; Sequence 3984, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3984
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-3984

Query Match          3.6%; Score 52.4; DB 6; Length 201;
Best Local Similarity 58.2%; Pred. No. 6.8e-07;
Matches 92; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 926 TTGTGAATATGAAGAAAGGTGTTTCAGGGTAACCTCTAACTTTCCGGACCCAGTGCAAA 985
DB 15 TTCAAGATGGCAAGTAAGGTTTTTCAGGAAATCAAGACTCTTCACACCTGTGTGA 74

QY 986 ACAATTTTCATCCCTCCCATCGTCCAGATATGTGGGGTTGTCCCCAGACATGGCACC 1045
DB 75 ACTCTAGACCCACCGTTACTGACTBGCTACCTTGAATTCACCCCCAGAGTTGGGTGC 134

QY 1046 AGAGGATAGCTTGAAGGTGAGCTCATTTGGTGGCAG 1083
DB 135 ACCAGATTGCCCTGAGGATGGAGGTTCTGGGCTGCGAG 172

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-10-813-588-1
Perfect score: 1464
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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq:*
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- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfileseq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1464	100.0	1464	3	US-09-691-344A-1 Sequence 1, Appli
2	1464	100.0	1620	3	US-09-691-344A-5 Sequence 5, Appli
3	1464	100.0	1761	3	US-09-691-344A-3 Sequence 3, Appli
4	1464	100.0	1768	3	US-09-691-344A-7 Sequence 7, Appli
5	449.8	30.7	1871	3	US-09-823-038A-43 Sequence 43, Appli
6	205.8	14.1	2310	3	US-10-191-436A-4 Sequence 4, Appli
7	205.8	14.1	2310	3	US-10-191-436A-6 Sequence 6, Appli
8	204	13.9	2328	3	US-10-191-436A-1 Sequence 1, Appli
9	204	13.9	2328	3	US-10-191-436A-3 Sequence 3, Appli
10	197.8	13.5	2310	3	US-10-191-436A-7 Sequence 7, Appli
11	197.8	13.5	2310	3	US-10-191-436A-9 Sequence 9, Appli
12	94.4	6.4	6893	3	US-09-054-272-37 Sequence 37, Appli
13	94.4	6.4	6914	3	US-09-949-002-6 Sequence 6, Appli
14	94.4	6.4	6987	3	US-09-949-002-231 Sequence 231, Appli
15	92.8	6.3	6909	2	US-08-804-196-1 Sequence 1, Appli
16	92.8	6.3	6909	2	US-08-858-340-1 Sequence 1, Appli
17	92.8	6.3	6909	3	US-08-746-111-26 Sequence 26, Appli
18	92.8	6.3	6909	3	US-08-454-353A-1 Sequence 1, Appli
19	92.8	6.3	6909	3	US-09-165-019-1 Sequence 1, Appli
20	81.6	5.6	7032	3	US-09-324-867-1 Sequence 1, Appli
21	80.6	5.5	6585	3	US-08-746-111-4 Sequence 4, Appli
22	78.4	5.4	4880	3	US-09-331-793-20 Sequence 20, Appli
23	78.4	5.4	2436	3	US-09-949-016-5790 Sequence 5790, Ap
24	78.4	5.4	4629	2	US-08-484-891-7 Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-09-691-344A-1
; Sequence 1, Application US/09691344A
; Patent No. 6743907
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6743907el Human Proteins and Polynucleotides
; FILE REFERENCE: Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/691,344A
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/183,583
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-691-344A-1

Query Match 100.0%; Score 1464; DB 3; Length 1464;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGACATCTAAGAAATATATCCCGGACCTACCCCAATCACACTGTGTCGAAAGACAAT	60
DB	1	ATGACATCTAAGAAATATATCCCGGACCTACCCCAATCACACTGTGTCGAAAGACAAT	60
QY	61	ACAGTACCAAGGGGAAAGACATGATTCGAGTTCGGAGATTTGGATATCGAATCCCAG	120
DB	61	ACAGTACCAAGGGGAAAGACATGATTCGAGTTCGGAGATTTGGATATCGAATCCCAG	120
QY	121	ACCTGTGCTTCGACTATCTTCTTCCAGCAGCTCTTCAGATCAATATGGTCCATACTGT	180
DB	121	ACCTGTGCTTCGACTATCTTCTTCCAGCAGCTCTTCAGATCAATATGGTCCATACTGT	180
QY	181	GGAAGTATGACTGTTCCTCCCAAGAACTCTTTGTTGAAACAAGTGAACCGTCCGCTTT	240
DB	181	GGAAGTATGACTGTTCCTCCCAAGAACTCTTTGTTGAAACAAGTGAACCGTCCGCTTT	240

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QY 241 GAGAGTGGATCCACACATTTCTGCGCGGGTTTTTGTGCTGACCTATGCGAGCAGCGACCAT 300
DB 241 GAGAGTGGATCCACACATTTCTGCGCGGGTTTTTGTGCTGACCTATGCGAGCAGCGACCAT 300
QY 301 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTAATTTGAAGACAGATACAGCAA 360
DB 301 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTAATTTGAAGACAGATACAGCAA 360
QY 361 TTCTGCCCGAGCTGGTGTAGAGAGCTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 420
DB 361 TTCTGCCCGAGCTGGTGTAGAGAGCTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 420
QY 421 TATAGAGATACCTCTTTATTTGTGCAAGCTGCCATCCATCGAGGAATAATTTCTGTGATGAA 480
DB 421 TATAGAGATACCTCTTTATTTGTGCAAGCTGCCATCCATCGAGGAATAATTTCTGTGATGAA 480
QY 481 CTAGGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGATCAGTCGATATGAAGGATTCG 540
DB 481 CTAGGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGATCAGTCGATATGAAGGATTCG 540
QY 541 GCCAATGGTGTCTTTTCAGCGGATGGTTCCTGTGCAGCAAGGATTTCTGTGTTACCTCC 600
DB 541 GCCAATGGTGTCTTTTCAGCGGATGGTTCCTGTGCAGCAAGGATTTCTGTGTTACCTCC 600
QY 601 AATGGTTGACGAGATCCTTTGAGTTTTGAAACCTGACGGGCAAAATCAGAGCTTTCTCTCA 660
DB 601 AATGGTTGACGAGATCCTTTGAGTTTTGAAACCTGACGGGCAAAATCAGAGCTTTCTCTCA 660
QY 661 TGGCAGTTCGTCAATGAGATGGAGACCAAGTTCACTGGTCTCTGCGCAAGCCGACTT 720
DB 661 TGGCAGTTCGTCAATGAGATGGAGACCAAGTTCACTGGTCTCTGCGCAAGCCGACTT 720
QY 721 CAGGACCAAGCCCATCATGGGCTTCGGCGCAGTAGCAACCAACCAACCAACGAGAG 780
DB 721 CAGGACCAAGCCCATCATGGGCTTCGGCGCAGTAGCAACCAACCAACCAACGAGAG 780
QY 781 TGGCTGAGATCGATTTGGGGAGAAAAGAAATAATACAGGAATTAGGACCAAGGATCT 840
DB 781 TGGCTGAGATCGATTTGGGGAGAAAAGAAATAATACAGGAATTAGGACCAAGGATCT 840
QY 841 ACACGTCGAACTTCACTTTTATGTTAAGGTTTGTGATGACTTCAAAACAAATAT 900
DB 841 ACACGTCGAACTTCACTTTTATGTTAAGGTTTGTGATGACTTCAAAACAAATAT 900
QY 901 TCTAAGTGGAGACCTATAAGGAATTTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 960
DB 901 TCTAAGTGGAGACCTATAAGGAATTTGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 960
QY 961 TCTAACTTTTGGGACCCAGTGCAAAACAAATTTTCATCCCTCCATCGTGGGCAAGATGTG 1020
DB 961 TCTAACTTTTGGGACCCAGTGCAAAACAAATTTTCATCCCTCCATCGTGGGCAAGATGTG 1020
QY 1021 CGGGTTGTCGCCAGATGCGCAGAGGATAGCTTTGAAGTGGAGCTCATTTGGTTC 1080
DB 1021 CGGGTTGTCGCCAGATGCGCAGAGGATAGCTTTGAAGTGGAGCTCATTTGGTTC 1080
QY 1081 CAGATTACAAAGTAAATGATTCATTTGTTGGCGCAAGCAAGTCAAAAGCAGGATGTT 1140
DB 1081 CAGATTACAAAGTAAATGATTCATTTGTTGGCGCAAGCAAGTCAAAAGCAGGATGTT 1140
QY 1141 TCAATTAAGAAAGATGAGACAAATCAAGGCGCCATTCCTCGGAAGAAACATCCACA 1200
DB 1141 TCAATTAAGAAAGATGAGACAAATCAAGGCGCCATTCCTCGGAAGAAACATCCACA 1200
QY 1201 GGAATTAACATTACAAAGTGGCTATTCCATTGGTGTCTCTTGTGTCCTGGTGTGCT 1260
DB 1201 GGAATTAACATTACAAAGTGGCTATTCCATTGGTGTCTCTTGTGTCCTGGTGTGCT 1260
QY 1261 GGAATGGGGATCTTTGAGCGCTTTAGAAAGAAAGAAAGAAAGGAGTCCGTATGGATCA 1320
DB 1261 GGAATGGGGATCTTTGAGCGCTTTAGAAAGAAAGAAAGAAAGGAGTCCGTATGGATCA 1320
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QY 1321 GCGAGGCTCAGAAAACAGACTGTTTGGAAAGCAGATTAAATATATCCCTTTGCCAGACATCAG 1380
DB 1321 GCGAGGCTCAGAAAACAGACTGTTTGGAAAGCAGATTAAATATATCCCTTTGCCAGACATCAG 1380
QY 1381 TCAGCTGAGTGTTCACCATCAGCTATGATTAATGAAGGAGATGACACAAAAGTTTGTATCTC 1440
DB 1381 TCAGCTGAGTGTTCACCATCAGCTATGATTAATGAAGGAGATGACACAAAAGTTTGTATCTC 1440
QY 1441 ATCACAAGTGATATGCGAGGTTAA 1464
DB 1441 ATCACAAGTGATATGCGAGGTTAA 1464
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RESULT 2

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US-09-691-344A-5
; Sequence 5, Application US/09691344A
; Patent No. 6743907
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6743907el Human Proteins and Polynucleotides
; FILE REFERENCE: Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/691,344A
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/183,583
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-691-344A-5
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Query Match 100.0%; Score 1464; DB 3; Length 1620;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTTCGAAAAAGACAATT 60
DB 157 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTTCGAAAAAGACAATT 216
QY 61 ACAGTACCAAGGGGAAAAGACTGATTCGAGGTTGGAGATTTGGATATCGAATCCCGAG 120
DB 217 ACAGTACCAAGGGGAAAAGACTGATTCGAGGTTGGAGATTTGGATATCGAATCCCGAG 276
QY 121 ACCTGTGCTTCTGACATATCTTCTTCCAGAGCTTTCAGATCAATATGCTCATCTGT 180
DB 277 ACCTGTGCTTCTGACATATCTTCTTCCAGAGCTTTCAGATCAATATGCTCATCTGT 336
QY 181 GGAAGTATGACTGTTTCCCAAGAACTCTTGTGGAACAACAAGTGAAGTAAACCGTCCGCTTT 240
DB 337 GGAAGTATGACTGTTTCCCAAGAACTCTTGTGGAACAACAAGTGAAGTAAACCGTCCGCTTT 396
QY 241 GAGAGTGGATCCCAATTTCTGCGCGGGTTTTTGTGACCTATGCGAGCAGGACCAT 300
DB 397 GAGAGTGGATCCCAATTTCTGCGCGGGTTTTTGTGACCTATGCGAGCAGGACCAT 456
QY 301 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTAATTTGAAGACAGATACAGCAA 360
DB 457 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTAATTTGAAGACAGATACAGCAA 516
QY 361 TTCTGCCCGAGCTGGTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 420
DB 517 TTCTGCCCGAGCTGGTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 576
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QY 421 TATAGAGATACCTCTTTATTTGTGCAAAAGCTGCCATCCATGACAGGAATAATTTGCTGATGAA 480
DB |||||
DB 577 TATAGAGATACCTCTTTATTTGTGCAAAAGCTGCCATCCATGACAGGAATAATTTGCTGATGAA 636
QY 481 CTAGGTGGCCAGATCAGTGTGCTTTACGCGAAAGGATCAGTGCATATGAGGGATCTTG 540
DB |||||
DB 637 CTAGGTGGCCAGATCAGTGTGCTTTACGCGAAAGGATCAGTGCATATGAGGGATCTTG 696
QY 541 GCCAATGGTGTCTTTTCGAGGGATGTTCCCTGTGACAGCAAGGATTTCTGTTTACTCTC 600
DB |||||
DB 697 GCCAATGGTGTCTTTTCGAGGGATGTTCCCTGTGACAGCAAGGATTTCTGTTTACTCTC 756
QY 601 AATGGTTGACAGATCCTTTGAGTTTGAACCTGACGGCAAAATCAGAGCTCTTCTCTCA 660
DB |||||
DB 757 AATGGTTGACAGATCCTTTGAGTTTGAACCTGACGGCAAAATCAGAGCTCTTCTCTCA 816
QY 661 TGGCAGTGGTCAATGAGAGTGAGACCAAGTTTCACTGTCTCTCTGGCCAGGCCGACTT 720
DB |||||
DB 817 TGGCAGTGGTCAATGAGAGTGAGACCAAGTTTCACTGTCTCTCTGGCCAGGCCGACTT 876
QY 721 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACAACCAACCAACCAAGAG 780
DB |||||
DB 877 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACAACCAACCAACCAAGAG 936
QY 781 TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAATAACAGGAATTAGGACCAAGGATCT 840
DB |||||
DB 937 TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAATAACAGGAATTAGGACCAAGGATCT 996
QY 841 ACACAGTGCNACTTCACTTTTATGTTAAGAGTTTGTGATGAACTTCAAAACAATAAT 900
DB |||||
DB 997 ACACAGTGCNACTTCACTTTTATGTTAAGAGTTTGTGATGAACTTCAAAACAATAAT 1056
QY 901 TCTAAGTGAAGACCTTATAAGAAATTTGAAATAATGAAGAAAGTGTTTCAGGGTAA 960
DB |||||
DB 1057 TCTAAGTGAAGACCTTATAAGAAATTTGAAATAATGAAGAAAGTGTTTCAGGGTAA 1116
QY 961 TCTAAGTGAAGACCTTATAAGAAATTTGAAATAATGAAGAAAGTGTTTCAGGGTAA 1020
DB |||||
DB 1117 TCTAAGTGAAGACCTTATAAGAAATTTGAAATAATGAAGAAAGTGTTTCAGGGTAA 1176
QY 1021 CGGGTGTCTCCCGACATGGCCAGAGGATAGCTTTGAGGTGAGCTCATTTGGTTGC 1080
DB |||||
DB 1177 CGGGTGTCTCCCGACATGGCCAGAGGATAGCTTTGAGGTGAGCTCATTTGGTTGC 1236
QY 1081 CAGATTACAAAGGTAATGATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1140
DB |||||
DB 1237 CAGATTACAAAGGTAATGATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1296
QY 1141 TCAACTAAGAAAGAGATGAGACAAATCACAAGGCCCATCCCTCGGAAGAAACATCCACA 1200
DB |||||
DB 1297 TCAACTAAGAAAGAGATGAGACAAATCACAAGGCCCATCCCTCGGAAGAAACATCCACA 1356
QY 1201 GGAATAAACAATTACAAAGGTGGCTATTCATTTGGTGTCTCTTGTGTTGTTGTTGTTGTT 1260
DB |||||
DB 1357 GGAATAAACAATTACAAAGGTGGCTATTCATTTGGTGTCTCTTGTGTTGTTGTTGTTGTT 1416
QY 1261 GGAATGGGGATCTTTTCAGCCTTTAGAAAGAGAAAGAAAGAGTCCGTATGATCA 1320
DB |||||
DB 1417 GGAATGGGGATCTTTTCAGCCTTTAGAAAGAGAAAGAAAGTCCGTATGATCA 1476
QY 1321 GGGAGGCTCAGAAAAAGAGATGTTGGAAGCAGATTAATAATATCCCTTTGCCAGACATCAG 1380
DB |||||
DB 1477 GGGAGGCTCAGAAAAAGAGATGTTGGAAGCAGATTAATAATATCCCTTTGCCAGACATCAG 1536
QY 1381 TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAGGAGATGACACAAAGTTAGATCTC 1440
DB |||||
DB 1537 TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAGGAGATGACACAAAGTTAGATCTC 1596
QY 1441 ATCACAAGTGATATGTCAGGTTAA 1464
DB |||||
DB 1597 ATCACAAGTGATATGTCAGGTTAA 1620
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RESULT 3

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US-09-691-344A-3
; Sequence 3, Application US/09691344A
; Patent No. 6743907
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6743907el Human Proteins and Polynucleotides
; FILE REFERENCE: LEX-0071-USA
; CURRENT APPLICATION NUMBER: US/09/691,344A
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/183,583
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-691-344A-3
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Query Match 100.0%; Score 1464; DB 3; Length 1761;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACACTGTTTGCAGAAAGACAATT 60
DB 298 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACACTGTTTGCAGAAAGACAATT 357
QY 61 ACAGTACCAAAAGGGGAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCCAG 120
DB 358 ACAGTACCAAAAGGGGAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCCAG 417
QY 121 ACCTGTGCTTTCGACTATCTTCTTCCAGCTCTTTCAGATCAATATGGTCCATCTGT 180
DB 418 ACCTGTGCTTTCGACTATCTTCTTCCAGCTCTTTCAGATCAATATGGTCCATCTGT 477
QY 181 GGAAGTATGACTGTTTCCCAAGAACTCTTTGTTGAAACACAAAGTAAACCGTCCGCTTT 240
DB 478 GGAAGTATGACTGTTTCCCAAGAACTCTTTGTTGAAACACAAAGTAAACCGTCCGCTTT 537
QY 241 GAGAGTGGATCCCAATTTCTGGCGGGGTTTTTTTGTGCTGACCTATTCGAGCAGCGACCAT 300
DB 538 GAGAGTGGATCCCAATTTCTGGCGGGGTTTTTTTGTGCTGACCTATTCGAGCAGCGACCAT 597
QY 301 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACAGCAA 360
DB 598 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATACAGCAA 657
QY 361 TTCTGCCAGCTGTTGTAGACACCTAGCAGAGACATTTCTGGGNAATATGTTAGATGA 420
DB 658 TTCTGCCAGCTGTTGTAGACACCTAGCAGAGACATTTCTGGGNAATATGTTAGATGA 717
QY 421 TATAGAGATACCTCTTTTATTTGTGCAAGCTGCCATCCATGACAGGAATAATTTGCTGATGA 480
DB 718 TATAGAGATACCTCTTTTATTTGTGCAAGCTGCCATCCATGACAGGAATAATTTGCTGATGA 777
QY 481 CTAGGTGGCCAGATCAGTGTGCTTTCAGCGAAAGGATCAGTGCATATGAGGGATCTTG 540
DB 778 CTAGGTGGCCAGATCAGTGTGCTTTCAGCGAAAGGATCAGTGCATATGAGGGATCTTG 837
QY 541 GCCAATGGTGTCTTTTCGAGGGATGTTCCCTGTGACAGCAAGGATTTCTGTTTACTCTC 600
DB 838 GCCAATGGTGTCTTTTCGAGGGATGTTCCCTGTGACAGCAAGGATTTCTGTTTACTCTC 697
QY 601 AATGGTTGACAGATCCTTTGAGTTTGAACCTGACGGGCAAAATCAGAGCTCTTCTCTCA 660
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898 AATGGTTCAGCAGATCCTTGGTGTGAAACCTGAGCGGCANATCAGAGCTTCTCTCA 957
661 TGGCAGTCGGTCAATGAGAGTGAGACCAAGTTTCACTGGTCTCTCGCCCAAGCCGACTT 720
958 TGGCAGTCGGTCAATGAGAGTGAGACCAAGTTTCACTGGTCTCTCGCCCAAGCCGACTT 1017
721 CAGGACCAAGGCCCATCATCGGCTTCGGCGCAGTAGCAACCAACCAACCAACCAAGAG 780
1018 CAGGACCAAGGCCCATCATCGGCTTCGGCGCAGTAGCAACCAACCAACCAACCAAGAG 1077
781 TGGCTGGAGATCGATTTGGGGGAGAAAGAAATACAGGAATAGGACCAAGATCT 840
1078 TGGCTGGAGATCGATTTGGGGGAGAAAGAAATACAGGAATAGGACCAAGATCT 1137
841 ACACAGTCGAATCTCAACTTTTATGTTAAGAGTTTGTGATGAATCTCAAAAACAATAAT 900
1138 ACACAGTCGAATCTCAACTTTTATGTTAAGAGTTTGTGATGAATCTCAAAAACAATAAT 1197
901 TCTAAGTGGAGACCTATAAAGGAATGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 960
1198 TCTAAGTGGAGACCTATAAAGGAATGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1257
961 TCTAAGTGGAGACCTATAAAGGAATGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1020
1258 TCTAAGTGGAGACCTATAAAGGAATGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1317
1021 CGGGTGTGCCCCCAGACATCGCACCAGAGATAGCTTTGAAGGTGAGCTCATTTGGTTGC 1080
1318 CGGGTGTGCCCCCAGACATCGCACCAGAGATAGCTTTGAAGGTGAGCTCATTTGGTTGC 1377
1081 CAGATTACAAGGTAAATGATTCATTGGTGTGGCGCAAGACAAGTCAAAGCAACCAAGTGT 1140
1378 CAGATTACAAGGTAAATGATTCATTGGTGTGGCGCAAGACAAGTCAAAGCAACCAAGTGT 1437
1141 TCAACTAAGAAAGAGATGAGCAATCACAAGGCCCATCCCTCGGAAGAAACATCCACA 1200
1438 TCAACTAAGAAAGAGATGAGCAATCACAAGGCCCATCCCTCGGAAGAAACATCCACA 1497
1201 GGAATAAACATTACAACGGTGGCTATTCCATTGGTGTCTCTTGTCTCTGGTGTGCT 1260
1498 GGAATAAACATTACAACGGTGGCTATTCCATTGGTGTCTCTTGTCTCTGGTGTGCT 1557
1261 GGAATGGGGATCTTTGAGCCTTTAGAAAGAAAGAAAGAAAGAAAGTCCGTATGATCA 1320
1558 GGAATGGGGATCTTTGAGCCTTTAGAAAGAAAGAAAGAAAGAAAGTCCGTATGATCA 1617
1321 GCGGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAAATATCCCTTTGCGACATCAG 1380
1618 GCGGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAAATATCCCTTTGCGACATCAG 1677
1381 TCAGCTGAGTTTACCATCAGCTATGATAATGAGAAGGAGATGACACAAAAGTTAGATCTC 1440
1678 TCAGCTGAGTTTACCATCAGCTATGATAATGAGAAGGAGATGACACAAAAGTTAGATCTC 1737
1441 ATCAAGTGATATGGCAGGTAA 1464
1738 ATCAAGTGATATGGCAGGTAA 1761
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RESULT 4
US-09-691-344A-7
; Sequence 7, Application US/09691344A
; Patent No. 6743907
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6743907el Human Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
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; FILE REFERENCE: LEX-0071-USA
; CURRENT APPLICATION NUMBER: US/09/691,344A
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,285
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/183,583
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1768
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-691-344A-7

Query Match 100.0%; Score 1464; DB 3; Length 1768;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTTTTCGGAAGACAAATT 60
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QY 61 ACAGTACCAAGGGGAAAGACTGATTCAGGTTTCGGAGATTTGGATATCGAATCCAG 120
DB 119 ACAGTACCAAGGGGAAAGACTGATTCAGGTTTCGGAGATTTGGATATCGAATCCAG 178
QY 121 ACCTGTGCTTCTGACTATCTTCTCTTCCAGAGCTTTCCAGATCAATATGTCATACTGT 180
DB 179 ACCTGTGCTTCTGACTATCTTCTTCCAGAGCTTTCCAGATCAATATGTCATACTGT 238
QY 181 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTAACACAAAGTGAAGTAAACCGTCCGCTTT 240
DB 239 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTAACACAAAGTGAAGTAAACCGTCCGCTTT 298
QY 241 GAGAGTGAATCCACATTTCTGGCCGCGGGTTTTTCTGACCTATGCGAGCAGACCAT 300
DB 299 GAGAGTGAATCCACATTTCTGGCCGCGGGTTTTTCTGACCTATGCGAGCAGACCAT 358
QY 301 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA 360
DB 359 CCAGATTAAATACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA 418
QY 361 TTCTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGTTAGATGGA 420
DB 419 TTCTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGTTAGATGGA 478
QY 421 TATAGAGATACCTCTTTATTTGTCAAAGCTGCCATCCATCGACGAAATAATTTGCTGATGAA 480
DB 479 TATAGAGATACCTCTTTATTTGTCAAAGCTGCCATCCATCGACGAAATAATTTGCTGATGAA 538
QY 481 CTAGGTGGCCAGATCAGTGTCTTCAAGCCGCAAGGGATCAGTCGATATGAAGGATCTG 540
DB 539 CTAGGTGGCCAGATCAGTGTCTTCAAGCCGCAAGGGATCAGTCGATATGAAGGATCTG 598
QY 541 GCCAATGGTGTCTTTTCGAGGGATGGTTCCCTGTGACAGCAAGGATTTCTGTTTACCTCC 600
DB 599 GCCAATGGTGTCTTTTCGAGGGATGGTTCCCTGTGACAGCAAGGATTTCTGTTTACCTCC 658
QY 601 AATGGTTGACGACAGATCCTTTGAGTTTGAACCTTGACGGGCAAAATCAGAGCTTCTTCTCA 660
DB 659 AATGGTTGACGACAGATCCTTTGAGTTTGAACCTTGACGGGCAAAATCAGAGCTTCTTCTCA 718
QY 661 TGGCAGTCGGTCAATGAGAGTGAGACCAAGTTTCACTGGTCTCTGCGCCAAAGCCGACTT 720
DB 719 TGGCAGTCGGTCAATGAGAGTGAGACCAAGTTTCACTGGTCTCTGCGCCAAAGCCGACTT 778
QY 721 CAGGACCAAGGCCCATCATCGGCTTCGGGGCAGTAGCAACCAACCAACCAACCAAGAG 780
DB 779 CAGGACCAAGGCCCATCATCGGCTTCGGGGCAGTAGCAACCAACCAACCAACCAAGAG 838
QY 781 TGGCTGGAGATCGATTTGGGGGAGAAAGAAATTAACAGGAATAGGACCAAGATCT 840
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Db 839 TGGCTGGAGATCGATTGGGGGAGAAAAAATAACAGGAATTAGGACCACAGGATCT 898
QY 841 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAACAATAAT 900
Db 899 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAACAATAAT 958
QY 901 TCTAAGTGAAGACCTATAAAGAAATGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 960
Db 959 TCTAAGTGAAGACCTATAAAGAAATGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 1018
QY 961 TCTAAGTGGGACCCAGTCGCAAAACAATTTTCATCCCTCCCATCTGGCCAGATATG 1020
Db 1019 TCTAAGTGGGACCCAGTCGCAAAACAATTTTCATCCCTCCCATCTGGCCAGATATG 1078
QY 1021 CGGGTTGTCCCCAGACATGGCCACAGAGGATAGCTTGAAGTGGAGCTCATTTGGTTGC 1080
Db 1079 CGGGTTGTCCCCAGACATGGCCACAGAGGATAGCTTGAAGTGGAGCTCATTTGGTTGC 1138
QY 1081 CAGATTACACAAGGTAATGATTCATTTGGTGTGGCGCAAGACAAAGTCAAAAGCACCACTGTT 1140
Db 1139 CAGATTACACAAGGTAATGATTCATTTGGTGTGGCGCAAGACAAAGTCAAAAGCACCACTGTT 1198
QY 1141 TCNACTAAGAAAGAGATGAGCAATCAACAGGCCCATCCCTCGGAAGAAACATCCACA 1200
Db 1199 TCNACTAAGAAAGAGATGAGCAATCAACAGGCCCATCCCTCGGAAGAAACATCCACA 1258
QY 1201 GGAATAAAACATTACAACGGTGGCTATTCCATTGGTGTCTCTTGTCTGCTGGTTTGTCT 1260
Db 1259 GGNATTAACATTTACAACGGTGGCTATTCCATTGGTGTCTCTTGTCTGCTGGTTTGTCT 1318
QY 1261 GGAATGGGATCTTTGACGCTTTAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1320
Db 1319 GGAATGGGATCTTTGACGCTTTAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1378
QY 1321 GCGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAATATATCCCTTTGCCAGACATCAG 1380
Db 1379 GCGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAATATATCCCTTTGCCAGACATCAG 1438
QY 1381 TCAGCTGAGTTTACCATCAGCTATGATATGATGAGAGGATGACACAAAGTTAGATCTC 1440
Db 1439 TCAGCTGAGTTTACCATCAGCTATGATATGATGAGAGGATGACACAAAGTTAGATCTC 1498
QY 1441 ATCACAAGTGATATGGCAGGTTAA 1464
Db 1499 ATCACAAGTGATATGGCAGGTTAA 1522
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RESULT 5

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US-09-823-038A-43
; Sequence 43, Application US/09823038A
; Patent No. 6797271
; GENERAL INFORMATION:
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Abernethy, Nevin
; APPLICANT: Onrust, Rene
; APPLICANT: Kumble, Anand
; APPLICANT: Murison, Greg
; TITLE OF INVENTION: Compositions Isolated From Stromal Cells
; FILE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1037c3
; CURRENT APPLICATION NUMBER: US/09/823,038A
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 1871
; TYPE: DNA
; ORGANISM: Mouse
US-09-823-038A-43
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Query Match 30.7%; Score 449.8; DB 3; Length 1871;
Best Local Similarity 84.0%; Pred. No. 1.5e-131;

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Matches 508; Conservative 0; Mismatches 97; Indels 0; Gaps 0;
QY 1 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTGTGTTCCGAAGAACAATT 60
Db 193 ATGACATCTAAGAAATTTATCCCGGACCTTACCCCAATTTACACTGTGTTGAAAGATCATC 252
QY 61 ACAGTACCAAAAGGGGAAAAAGACTGATTTCTGAGGTTGGGAGATTTGAGATATCGAATCCCAG 120
Db 253 ACAGTACCAAAAGGGGAAAGAGACTTATTTCTGAGGTTGGGAGATTTGAACTTGAATCCAAG 312
QY 121 ACTGTGCTTCTGACTATCTTCTTCCACAGCTCTTTCAGATCAATATGTTCCATCTGT 180
Db 313 ACTGTGCTTCTGACTATCTTCTTCCACAGCTGCAACAGATCAGTATGTTCCATATGT 372
QY 181 GGAAGTATCAGTCTTCCCAAGAACTCTTTGTTGAAACACAAGTGAAGTAAACCGTCCGCTTT 240
Db 373 GGAAGTATGAGTCTTCCCAAGAACTCTCGGCTGAACCTCAACGAAGTGACTGTCTCTTTC 432
QY 241 GAGAGTGAATCCCACTATTTCTGGCCGGGGTTTTTGTGCTGACCTATTCGAGCAGCAGCCAT 300
Db 433 AAGAGTGAATCTCACATTTCTGGCCGGGGCTTTCTGCTGACCTTACGCCAGCAGTACCAT 492
QY 301 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATATTTGAAGACAGAAATACAGAAA 360
Db 493 CCAGATTTAATAACCTGTTTGGAAACGAGCAGCCATTTATTCGAGGAAAAATAACAGAAA 552
QY 361 TTCTGCCACAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGTTAGATGGA 420
Db 553 TTCTGCCACAGCTGTTGTAGAGACATAGCAGGAGATTTCTGGGAATATCAAAAGATGGT 612
QY 421 TATAGAGATACCTCTTTTATTTGTGCAAGCTGCCATCCATCGCAGGAATAATTTGCTGATGA 480
Db 613 TACAGAGATACCTCTTTTATTTGTGCAAGCTGCCATCCACGCGAGGATCATCAGATGAA 672
QY 481 CTAGTGGCCAGATCAGTGTCTTTCAGCCAAAGGGATCAGTCGATATGAAGGATCTTG 540
Db 673 CTAGTGGCCACATCAACTTGTCTTTCAGACAAAGGGATAGTCACTATGAAGGACTCCTG 732
QY 541 GCAATGTTGTTCTTTTCGAGGGATGTTCCCTGTCAGACAAGCGATTTCTGTTTACCTCC 600
Db 733 GCAATGTTGTTCTTTCCCGGATGTTCTTTGTCGAAAGGAGATTTCTTTTACACC 792
QY 601 AATGG 605
Db 793 CCAGG 797
```

RESULT 6

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US-10-191-436A-4
; Sequence 4, Application US/10191436A
; Patent No. 6900031
; GENERAL INFORMATION:
; APPLICANT: Tasuku Honjo
; APPLICANT: Kei Tashiro
; APPLICANT: Kazuhiro Kobuke
; TITLE OF INVENTION: A NOVEL POLYPEPTIDE ESDN, POLYNUCLEOTIDES ENCODING THE POLYPEPTIDE
; FILE OF INVENTION: UTILITY OF THE POLYPEPTIDE
; FILE REFERENCE: Q70993
; CURRENT APPLICATION NUMBER: US/10/191,436A
; CURRENT FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2310
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(198)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (199)..(2310)
; FEATURE:
```

/ NAME/KEY: CDS
/ LOCATION: (1)..(2310)
US-10-191-436A-4

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Query Match      14.1%; Score 205.8; DB 3; Length 2310;
Best Local Similarity 54.0%; Pred. No. 3.9e-54;
Matches 482; Conservative 0; Mismatches 387; Indels 24; Gaps 2;

QY 210 GTTGAACACAAAGTGAAGTAAACCGTCCGCTTTGAGAGTGGATCCACATTTCTGGCCGGGG 269
DB 468 GTCCAAAGGCGAGTGAAGTCAAGTGTCTGTTTCATGAGTGGAAACCCATGCTGCTGGCGAGG 527

QY 270 TTTTGTGTCGACCTATGCGAGCGAGCCACCATCCAGATTTTAATAACAATGTTTGGAAACGAGC 329
DB 528 ATTTTGGCTTCATACCTCAGTTATAGATAAAGAAGATTTAATCACTGTTTGGATACTGT 587

QY 330 TAGCCATATTGGAAGACAGAAATACAGCAAAATCTGCCAGCTGGTGTGTAGACACGTAGC 389
DB 588 ATCTAAATTTTGGAAACCGAGTTCAGTAAGTACTGCCAGCTGGCTGCTTTTGGCCTTT 647

QY 390 AGGAGCATTTCTGGGAATATGTTAGATGATAGATACCTCTTTATTGTGCAAGC 449
DB 648 TGCTGAATAATCTGGAAACAATTCCTCATGATACAGAGATTTCTCACCATTGTTATGGC 707

QY 450 TGCCATCCATGCGAGGAATAATGCTGATGAATAGTGGCCAGATCAGTGTGCTTCAGCG 509
DB 708 TGGNAATCCATGCGAGGAGTAGTGTCAAAACGTCGTGGGTGGCCAAATCAGCATTTGTGATTAG 767

QY 510 CAAAGGATCAGTCGATATGAAGGGATTCCTGCGCAATGTTGCGAGAGTCTTTTCAGAGGATGGTTC 569
DB 768 CAAAGGACCCCATATTATGAAGCTCTTTGGCCAAACAATGTCACTTCCACGGTGGGATA 827

QY 570 CCTGTGACAGCAAGCATTTCTGTTTACCTCCATGTTGCGAGAGTGGCTGGAGATCGATTT 629
DB 828 CTATCTGCAAGTCTGTTTACATTTAAGACAAAGTGTGCTATGGGACTCTGGGATGGA 887

QY 630 ACCTGACGGG-----CAAATCAGAGCTTTCTTCCATGTCAGTGGCAGTCCGTCATGA 677
DB 888 GTCTGGTGTGATGTCGCGATCCCAAGATAACAGCATCTCTGCACTGGAGTGGACTGACCA 947

QY 678 GAGTGGAGACCAAGTTCACTGCTCTCTGGCCCAAGCCCGACTTCAGGACCAAGCCCATC 737
DB 948 CATGGGCGAGGAGAACAGCTGGACAGCGGAGAGCGCGCTGAGAAAAACCCGGGCTCC 1007

QY 738 ATGGGCTTTCGGGCGACAGTAGTAGCAACACCAACCAACAGAGTGGCTGGAGATCGATTT 797
DB 1008 CTGGCTGCTTTTGGCCACTGATGAGCATC-----AGTGGCTGCAAGTAGACCT 1055

QY 798 GGGGAGAAAAAAGAAATAACAGGAATTAAGGACCAAGGATCTACAGTGCAGACTTCAA 857
DB 1056 TAAACAGGAGAGAAGATAACAGGTATCGTAACCACTGGGTCTACCATGATAGAACACAG 1115

QY 858 CTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAAACAATAATTTCTAAGTGGAGACCTTA 917
DB 1116 TTACTATGTGTCTGCCTACAGAGTCTGTATACGTGACGATGGGCGAGAGATGGACTGTGTA 1175

QY 918 TAAAGGAATTTGTGAATAATGAAGAAAAAGGTGTTTTCAGGGTAACTCTTAACGTGGAAGACCTTA 977
DB 1176 CAGAAACCTGGTGGACCAAGGACAGATATTTCAAGGAAAAACAAGATTATACAGGA 1235

QY 978 AGTGCAAAACAATTTCACTCCCTCCCATCGTGGCCAGATATGTCGGGTTGTCCCCCAGAC 1037
DB 1236 TGTTCGTAAATACTTTTGGCCACCAATTTATTCAGAGTTTCAATAGAGTGAACCTGTCTCA 1295

QY 1038 ATGGCACAGAGGATAGCTTGAAGGTGAGCTCATTTGGTGGCAGATTACAC 1090
DB 1296 GTGGCAACAGAAAAATTGCCATGAAGTGAAGTCTGCTCGGATGTTCAGTGTTC 1348
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RESULT 7
US-10-191-436A-6
; Sequence 6, Application US/10191436A
; Patent No. 6900031

/ GENERAL INFORMATION:

/ APPLICANT: Tasuku Honjo
/ APPLICANT: Kei Tashiro
/ APPLICANT: Kazuhiro Kobuke
/ TITLE OF INVENTION: A NOVEL POLYPEPTIDE ESDN, POLYNUCLEOTIDES ENCODING THE POLYPEPTIDE
/ TITLE OF INVENTION: UTILITY OF THE POLYPEPTIDE
/ FILE REFERENCE: Q70993
/ CURRENT APPLICATION NUMBER: US/10/191,436A
/ CURRENT FILING DATE: 2002-07-10
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 2310
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-10-191-436A-6

```
Query Match      14.1%; Score 205.8; DB 3; Length 2310;
Best Local Similarity 54.0%; Pred. No. 3.9e-54;
Matches 482; Conservative 0; Mismatches 387; Indels 24; Gaps 2;

QY 210 GTTGAACACAAAGTGAAGTAAACCGTCCGCTTTGAGAGTGGATCCACATTTCTGGCCGGGG 269
DB 468 GTCCAAAGGCGAGTGAAGTCAAGTGTCTGTTTCATGAGTGGAAACCCATGCTGCTGGCGAGG 527

QY 270 TTTTGTGTCGACCTATGCGAGCGAGCCACCATCCAGATTTTAATAACAATGTTTGGAAACGAGC 329
DB 528 ATTTTGGCTTCATACCTCAGTTATAGATAAAGAAGATTTAATCACTGTTTGGATACTGT 587

QY 330 TAGCCATATTGGAAGACAGAAATACAGCAAAATCTGCCAGCTGGTGTGTAGACACGTAGC 389
DB 588 ATCTAAATTTTGGAAACCGAGTTCAGTAAGTACTGCCAGCTGGCTGCTTTTGGCCTTT 647

QY 390 AGGAGCATTTCTGGGAATATGTTAGATGATAGATACCTCTTTATTGTGCAAGC 449
DB 648 TGCTGAATAATCTGGAAACAATTCCTCATGATACAGAGATTTCTCACCATTGTTATGGC 707

QY 450 TGCCATCCATGCGAGGAATAATGCTGATGAATAGTGGCCAGATCAGTGTGCTTCAGCG 509
DB 708 TGGNAATCCATGCGAGGAGTAGTGTCAAAACGTCGTGGGTGGCCAAATCAGCATTTGTGATTAG 767

QY 510 CAAAGGATCAGTCGATATGAAGGGATTCCTGCGCAATGTTGCGAGGATGGTTC 569
DB 768 CAAAGGACCCCATATTATGAAGCTCTTTGGCCAAACAATGTCACTTCCACGGTGGGATA 827

QY 570 CCTGTGACAGCAAGCATTTCTGTTTACCTCCATGTTGCGAGAGATCCCTTGTGATTTGA 629
DB 828 CTATCTGCAAGTCTGTTTACATTTAAGACAAAGTGTGCTATGGGACTCTGGGATGGA 887

QY 630 ACCTGACGGG-----CAAATCAGAGCTTTCTTCCATGTCAGTGGCAGTCCGTCATGA 677
DB 888 GTCTGGTGTGATGTCGCGATCCCAAGATAACAGCATCTCTGCACTGGAGTGGACTGACCA 947

QY 678 GAGTGGAGACCAAGTTCACTGCTCTCTGGCCCAAGCCCGACTTCAGGACCAAGCCCATC 737
DB 948 CATGGGCGAGGAGAACAGCTGGACAGCGGAGAGCGCGCTGAGAAAAACCCGGGCTCC 1007

QY 738 ATGGGCTTTCGGGCGACAGTAGTAGCAACACCAACCAACAGAGTGGCTGGAGATCGATTT 797
DB 1008 CTGGCTGCTTTTGGCCACTGATGAGCATC-----AGTGGCTGCAAGTAGACCT 1055

QY 798 GGGGAGAAAAAAGAAATAACAGGAATTAAGGACCAAGGATCTACAGTGCAGACTTCAA 857
DB 1056 TAAACAGGAGAGAAGATAACAGGTATCGTAACCACTGGGTCTACCATGATAGAACACAG 1115

QY 858 CTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAAACAATAATTTCTAAGTGGAGACCTTA 917
DB 1116 TTACTATGTGTCTGCCTACAGAGTCTGTATACGTGACGATGGGCGAGAGATGGACTGTGTA 1175

QY 918 TAAAGGAATTTGTGAATAATGAAGAAAAAGGTGTTTTCAGGGTAACTCTTAACGTGGAAGACCTTA 977
DB 1176 CAGAAACCTGGTGGACCAAGGACAGATATTTCAAGGAAAAACAAGATTATACAGGA 1235

QY 978 AGTGCAAAACAATTTCACTCCCTCCCATCGTGGCCAGATATGTCGGGTTGTCCCCCAGAC 1037
DB 1236 TGTTCGTAAATACTTTTGGCCACCAATTTATTCAGAGTTTCAATAGAGTGAACCTGTCTCA 1295

QY 1038 ATGGCACAGAGGATAGCTTGAAGGTGAGCTCATTTGGTGGCAGATTACAC 1090
DB 1296 GTGGCAACAGAAAAATTGCCATGAAGTGAAGTCTGCTCGGATGTTCAGTGTTC 1348
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Db 727 GCAGGAGTAGTGTCAAAACACGTTGGGCGGCCAAATCAGTGTGTGTAATAGTAAAGTAT 786
Qy 520 AGTCGATATGAAGGATCTGGCCAAATGGTGTCTTTTCGAGGAGATGGTTCCCTGTGTCAGAC 579
Db 787 CCTATTATGAAGTCTTTGGCTTAAACAGTCAATCTGTGTGGACACTTATCTACA 846
Qy 580 AAGCGATTTCTGTTTACCTCCAAATGGTTCAGCAGATCCTTGTAGTTTGTGAACCTGACGG 639
Db 847 AGTCCTTTTACATTTAAGACAAGTGGATGTTATGGAACACTGGGGATGGAGTCTGGTGTG 906
Qy 640 -----CAAAATCAGAGCTTCTTCCTCATGGCAGTCGCTCAATGAGAGTGGAGAC 687
Db 907 ATCCGCGATCCTCAAAATAACAGCATCATCTGTGCTGGAGTGGAGCTGACCAACAGGGCAA 966
Qy 688 CAAGTTTCACCTGGTCTCTCGGCCAAGCCGACTTTCAGGACCAAGCCCATCATGGGCTTCG 747
Db 967 GAGAACAGTTTGGAAACCCAAAAGCCAGGCTGAAAAACCTGACCGCTTGGGCTGCT 1026
Qy 748 GGCAGCAGTAGCAACCAACCAACCAACGAGAGTGGCTGGAGATCGATTTTGGGGGAGAAA 807
Db 1027 TTTGGCCACTGATGAATACC-----AGTGGTTACAAATAGATTTGAATAAGGAA 1074
Qy 808 AAGAAATAACAGGAATTAGGACCAACAGGATCTACACAGTCGAACCTTCAACTTTTATGTT 867
Db 1075 AAGAAATAACAGGCATTTAACCACCTGGATCCACCATGGTGGAGCACAATTTACTATGTG 1134
Qy 868 AAGAGTTTGTGTGATGAATTTCAAAAACAATAATTTCTAAGTGGAGAGACCTATAAGGAAT 927
Db 1135 TCTGCTTACAGATTCCTGTACAGTGTATGATGGGAGAAATGGACTGTGTACAGAGCCT 1194
Qy 928 GTGAATAATGAAGAAAGGTGTTTTCAGGGTAACCTTAACTTTCCGGACCCAGTGCAGAAC 987
Db 1195 GGTGTGGAGCAAGATAAGATATTTCAAGGAGAAACAAAGATTTATCACAGGATGTGCGTAAT 1254
Qy 988 AATTTCATCCCTCCATCGTGGCCAGATATGTGGGGTGTGTCCTCCAGACATGGCACCAG 1047
Db 1255 AACTTTTGGCCACCAATTTATTCACGTTTTATTAGAGTGAATCCTACCCAAATGGCAGCAG 1314
Qy 1048 AGGATAGCTTGAAGGTGGAGCTCATTTGGTTGCCAGATTA 1087
Db 1315 AAAATGCCATGAATGGAGCTGCTCGGATGTCAAGTTTA 1354

RESULT 10

US-10-191-436A-7

; Sequence 7, Application US/10191436A

; Patent No. 6900031

; GENERAL INFORMATION:

; APPLICANT: Tasuku Honjo

; APPLICANT: Kei Tashiro

; APPLICANT: Kazuhiro Kobuke

; TITLE OF INVENTION: A NOVEL POLYPEPTIDE BSDN, POLYNUCLEOTIDES ENCODING THE POLYPEPTIDE

; FILE REFERENCE: Q70993

; CURRENT APPLICATION NUMBER: US/10/191.436A

; CURRENT FILING DATE: 2002-07-10

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 2310

; TYPE: DNA

; ORGANISM: Rattus rattus

; FEATURE:

; NAME/KEY: sig_peptide

; LOCATION: (1)..(198)

; FEATURE:

; NAME/KEY: mat_peptide

; LOCATION: (199)..(2310)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(2310)

US-10-191-436A-7

Query Match 13.5%; Score 197.8; DB 3; Length 2310;
Best Local Similarity 53.4%; Pred. No. 1.4e-51;
Matches 477; Conservative 0; Mismatches 392; Indels 24; Gaps 2;

Qy 210 GTTGAACACAGTGAAGTAAACCGTTCGGCTTCGAGAGTGGATCCACATTTCTTGGCGGG 269
Db 468 GTCCAAAGCAGTGAATCACAGTGTCTTCATGAGTGGAAATCCATGCTTCTGGTGGAGG 527
Qy 270 TTTTGTCTGACCTATGCGAGCAGCAGCCATCCAGATTTTAAATAACATGTTTGGAAACGAGC 329
Db 528 ATTTTGGCTTCTTACTCAGTTATAGATAAACAAGATTTAATCACATGTTTGGATACTGT 587
Qy 330 TAGCCATTATTTGAAGACAGAAATAACAGAAAATCTCCAGAGCTGGTGTAGAGACGTAGC 389
Db 588 ATCTAATTTTGGAAACCTGAGTTCAAGTAAGTACTGCCAGCTGGCTGTCTGCTGCTTT 647
Qy 390 AGGAGACATTTCTGGGAATATGTTAGATAGATATAGATACCTCTTTTATGTGCAAGC 449
Db 648 TGCTGAATATCTGGAAACGATTCCTCATGATATAGATTTTTCACCGCTGTGTATGGC 707
Qy 450 TGCATCTCCATGCAAGGAATAATTTGCTCTGATGAATCTAGGTGGCCAGATCAGTGTGCTTCAGCG 509
Db 708 TGGAAATCCATGCAAGGAGTAGTGTGAGATGCTGGCTGGCCAAATCAGCGTGTGATTAG 767
Qy 510 CAAAGGATCAGTCGATAGAGGGAATCTCGGCCAATGTTGTTCTTTCGAGGAGTGGTTC 569
Db 768 CAAAGGCACCCCATATATACGAAAGTTCTTTTGGCCAAACAATGTCACTTCCATGGTGGGATA 827
Qy 570 CCTGTCCAGCAACGGATTTCTGTTTACCTCCAAATGTTGCGAGCAGATCCTTTGAGTTTGA 629
Db 828 CTTATCTACAGTCTGTGTTTACATTTAAGACAAGTGTGTTGCTATGGGACTCTAGGATGGA 887
Qy 630 ACCTGACGGG-----CAAAATCAGAGCTTCTTCTCATGGCAGTCCGTCAATGA 677
Db 888 GTCAGGTGTGATCGCCGATCCCGAGATAACAGCATCATCTGTATGAGTGGACTGACCA 947
Qy 678 GAGTGGAGACCAAGTTTCACTGTCTCTGGCCAAAGCCGACTTCAGGACCAAGGCCCATC 737
Db 948 CATGGGGCAGGAGAACAGCTGGAAACCCGAGAAAGGCCAGGCTGAGAAAACCGGGGCTCC 1007
Qy 738 ATGGGCTTGGGGCAGTAGCAACCAACCAACAGAGAGTGGCTGGAGATCGATTT 797
Db 1008 CTGGGCTGCTTTTGGCCACTGATGAGATC-----AGTGGCTGCAATTTGACCT 1055
Qy 798 GGGGAGAAAAGAAAATAACAGGAATTAGGACCAAGGATCTACACAGTTCGAACTTCAA 857
Db 1056 TAATAAGGAGAGAGAGATAACAGGCATCGTAAACCACTGGATCTACCTGTATAGACACAA 1115
Qy 858 CTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAACAATAATTTCTAAGTGGAGACCTA 917
Db 1116 TTACTATGTCTCTGCCCTACAGAGTTCTGTACAGTGCAGTGGGAGAAAATGGAATGTGTA 1175
Qy 918 TAAAGGAATTTGTAATAATCAAGAAAAGGTGTTTCAGGGTAACCTTAACTTTTCGGGACCC 977
Db 1176 CAGAGACCTTGTGGCTCAGGACAGATATTTCAAGGAAACAAAGATTTATCACAAGGA 1235
Qy 978 AGTGCAAAAACAATTTTCACTCCCTCCATCGTGGCCAGATATGTGGGGTGTGTCCTCCAGAC 1037
Db 1236 TGTTGTAATAACTTTTTTGGCCACCAATTAATTGCAACGTTTCAATTAGAGTGAACCCCTGTCCA 1295
Qy 1038 ATGGCACCAGAGGATAGCTTGAAGTGGAGCTCATTTGGTTGCCAGATTACAC 1090
Db 1296 GTGGCAACAGAAAATTCGCATGAAGTGGAAATGCTGGGATGTCAAGTTCACTC 1348

RESULT 11

US-10-191-436A-9

; Sequence 9, Application US/10191436A

; Patent No. 6900031

; GENERAL INFORMATION:

; APPLICANT: Tasuku Honjo

; APPLICANT: Kei Tashiro

RESULT 12

; Sequence

: GENERAL

REF. :
APPL. :

APPL. -
ADPT. -

APPL. TITL

NUMBER ; TITLE

CORRECTION

;

; STS

; 218

MEI ;

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NAN

REC
DEF

TEST :

; TEL

; INFORM

; LEN

; STTS

MOLEC

NAME: _____

OTHER:

440

Query: ma
Best Loc

SAITTA

5

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57

Qy

D'b e

Qy

Db 6386 AATGCCAGGAGCGTGTGAATGCTTGGCAAGCCAAAGGCAAAACAATAAGC-----AG 6439
Qy 781 TGGCTGAGATCGAATTTGGGGGAGAAAAAAGAAATAACAGGAATTAGGACCAACAGGATCT 840
Db 6440 TGGCTAGAAATTGATCTACTCAAGATCAAGAGATAACGGCAATTATAACACAGGCTGC 6499
Qy 841 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGTGATGAACCTTCAAAAAACAATAAT 900
Db 6500 AAGTCTCTGCTCTGAAATGTATGTAAGAGCTATACCACTACAGTACAGTACAGGAGGA 6559
Qy 901 TCTAAGTGGAGACCTTAAAGGAATGTGAATAATGAAGAAAGGTGTTTCAGGCTAAC 960
Db 6560 GTGGAATGGAAACATACAGGCTGGAATCTCTCATGTGTGACAGAAATTTTGAAGGAAT 6619
Qy 961 TCTAACTTTTGGGACCCAGTGCACAAATTTTCATCCCTCCCATCGTGGCCAGATATGTG 1020
Db 6620 ACTAATACCAAGGACATGTGAAGAACTTTTCAACCCCAATCATTTCCAGTTATC 6679
Qy 1021 CGGGTTGTCCTCCAGACATGGCACAGAGATAGCTTGAAGGTGAGCTCATTTGGTTGC 1080
Db 6680 CGTGTCAATCTTAAACATGGAATCAAGTATTGCACTTCGCTGGAACCTCTTTGGCTGT 6739
Qy 1081 CAGATT 1086
Db 6740 GATATT 6745

RESULT 13
US-09-949-002-6
; Sequence 6, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 6914
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-6

Query Match 6.4%; Score 94.4; DB 3; Length 6914;
Best Local Similarity 51.2%; Pred. No. 1.6e-18;
Matches 249; Conservative 0; Mismatches 231; Indels 6; Gaps 1;
Qy 501 AATGGTTGCAGCAGATCCTTGAGTTTGAACCTTACCGGCAATATCAGAGCTTCTTCTCA 660
Db 6287 AATGGATGTTTCCACACCCCTGGGTATGGAATAATGGAAGATAGAAAACAAGCAATCACA 6346
Qy 661 TGGCAGTCGGTCAATGAGGTGGAGACCAAGTTCACCTGCTCTGCGCAAGCCCGACTT 720
Db 6347 GCTTCTTCTGTTAAGAAATCTTGTGGGAGATTACTGGGACCCCTTCCGTCCTGCTG 6406
Qy 721 CAGGACCAAGCCCATCATGGGCTTCGGGGAGACAGTAGCAACCAACCAACCAAGGAGAG 780
Db 6407 AATGCCAGGAGCGTGTGAATGCTGCGCAAGCCCAAGGCAACCAACAATAAGC-----AG 6460
Qy 781 TGGCTGAGATCGAATTTGGGGGAGAAAAAAGAAATAACAGAAATTAGGACCAAGGATCT 840
Db 6461 TGGCTAGAAATTTGATCTACTCAAGATCAAGAAGATAACGGCAATTATAACACAGGGCTGC 6520
Qy 841 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGTGATGAACCTTCAAAAAACAATAAT 900
Db 6521 AAGTCTCTGCTCTGGAATGTATGTAAGAGCTATACCACTCCTACAGTACAGGAGGA 6580

Qy 901 TCTAAGTGGAGACCTTATAAGGAATTTGTAATATATGAAGAAAGGTGTTTCAGGCTAAC 960
Db 6581 GTGGAATGGAAACCACTACAGGCTGAAATCCTCATGTGTGCAAGAAATTTTGAAGGAAT 6640
Qy 961 TCTAATCTTTGGGAGCCAGTGCACAAACAATTTTCATCCCTCCCATCGTGGCCAGATATGTG 1020
Db 6641 ACTAATACCAAGGACATGTGAAGAACTTTTCAACCCCAATCATTTCCAGGTTTATC 6700
Qy 1021 CGGGTTGTCCTCCAGACATGGCACAGAGATAGCTTGAAGGTGAGCTCATTTGGTTGC 1080
Db 6701 CGTGTCAATCTTAAACATGGAATCAAGTATTGCACTTCGCTGGAACCTCTTTGGCTGT 6760
Qy 1081 CAGATT 1086
Db 6761 GATATT 6766

RESULT 14
US-09-949-002-231
; Sequence 231, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 6987
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-231

Query Match 6.4%; Score 94.4; DB 3; Length 6987;
Best Local Similarity 51.2%; Pred. No. 1.6e-18;
Matches 249; Conservative 0; Mismatches 231; Indels 6; Gaps 1;
Qy 601 AATGGTTGCAGCAGATCCTTGAGTTTGAACCTTACCGGCAATATCAGAGCTTCTTCTCA 660
Db 6135 AATGGATGTTTCCACACCCCTGGGTATGGAATAATGGAAGATAGAAAACAAGCAATCACA 6194
Qy 661 TGGCAGTCGGTCAATGAGGTGGAGACCAAGTTCACCTGCTCTGCGCAAGCCCGACTT 720
Db 6195 GCTTCTTCTGTTAAGAAATCTTGTGGGAGATTACTGGGACCCCTTCCGTCCTGCTG 6254
Qy 721 CAGGACCAAGCCCATCATGGGCTTCGGGGAGACAGTAGCAACCAACCAACCAAGGAGAG 780
Db 6255 AATGCCAGGAGCGTGTGAATGCTTGGCAAGCCCAAGGCAACCAACAATAAGC-----AG 6308
Qy 781 TGGCTGAGATCGAATTTGGGGGAGAAAAAAGAAATAACAGGAATTAGGACCAAGGATCT 840
Db 6309 TGGCTAGAAATTTGATCTACTCAAGATCAAGAGATAACGGCAATTATAACACAGGGCTGC 6368
Qy 841 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGTGATGAACCTTCAAAAAACAATAAT 900
Db 6369 AAGTCTCTGCTCTGAAATGTATGTAAGAGCTATACCACTCCTACAGTACAGGAGGA 6428
Qy 901 TCTAAGTGGAGACCTTATAAGGAATTTGTAATAATGAAGAAAGGTGTTTTCAGGGTAAAC 960
Db 6429 GTGGAATGGAAACCATACAGGCTGAAATCCTCCATGTGTGCAAGATTTTGAAGGAAT 6488
Qy 961 TCTAATCTTTGGGAGCCAGTGCACAAACAATTTTCATCCCTCCCATCGTGGCCAGATATGTG 1020
Db 6489 ACTAATACCAAGGACATGTGAAGAACTTTTCAACCCCAATCATTTCCAGGTTTATC 6548
Qy 1021 CGGGTTGTCCTCCAGACATCGCACAGAGATAGCTTGAAGGTGAGCTCATTTGGTTGC 1080

Db 6549 CGTGTCTATCTCTAAACATGSAATCAAAGTATTGCACTTCGCTCGGAACCTTTTGGCTGT 6608
Qy 1081 CAGATT 1086
Db 6609 GATATT 6614

RESULT 15
US-08-804-196-1
; Sequence 1, Application US/08804196
; Patent No. 5874256
; GENERAL INFORMATION:
; APPLICANT: Bertina, Rogier
; APPLICANT: Reitsma, Pieter
; TITLE OF INVENTION: A method for diagnosing an increased
; TITLE OF INVENTION: risk for thrombosis or a genetic defect causing
; TITLE OF INVENTION: thrombosis and kit for use with the same.
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5874256el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,196
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/454,353
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 948-7400
; TELEFAX: (301) 948-9751
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6909 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
US-08-804-196-1

Query Match 6.3%; Score 92.8; DB 2; Length 6909;
Best Local Similarity 51.0%; Pred. No. 5.3e-18;
Matches 248; Conservative 0; Mismatches 232; Indels 6; Gaps 1;
Qy 601 AATGGTTGACAGATCCTTTGAGTTTGAACCTGACGGGCAATCAGAGCTTCTCTCTCA 660
Db 6280 AATGGATGTTCCACACCCCTGGGTATGGAATGGAAGATGAACAAACAGCAATCACA 6339
Qy 661 TGGCAGTCGGTCAATGAGAGTGAGACCAAGTTTCACTGGTCTCTCTGGCCAAAGCCGACTT 720
Db 6340 GCTTCTTCTGTTAAGAAATCTTGGTGGGAGATTACTTGGGAACCTTCCGTGCCCGTCTG 6399
Qy 721 CAGGACCAAGCCCATCATCGGCTTCGGGGCAGTAGCAACCAACCAACCAACAGAG 780
Db 6400 AATGCCCAAGGACGTGTGAATGCTGCAAGCCCAAGCAACCAATAGC-----AG 6453
Qy 781 TGGCTGGAGATCGATTGGGGGAGAAAAAGAAATAACAGAAATTAGGACCAAGGATCT 840
Db 6454 TGGCTAGAATTTGATCTTACTCAGATCAAGAGATTAACGCAATTTATACAGGGCTGC 6513
Qy 841 ACACAGTCGAACCTTCACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAAAACAATAAT 900

Db 6514 AAGTCTCTGTCTCTGAAATGTATGTAAAGAGCTATACCATCCACTACAGTGACGAGGA 6573
Qy 901 TCTAAGTGGAGACCTATATAAGGAATGTGAATAATGAAGAAAGGTGTTTCAGGGTAAC 960
Db 6574 GTGGAATGGAAACCATACACAGGCTGAAATCCTCCATGGTGGACAAGATTTTGAAGGAAAT 6633
Qy 961 TCTAACTTTTGGGACCCAGTGCAAAACAATTTTCATCCCTCCCATCGTGGCCAGATATGTG 1020
Db 6634 ACTAATACCAAGACATGTGAAGAACTTTTCAACCCCAATCATTTCCAGGTTTATC 6693
Qy 1021 CGGGTTGTCCCCAGACATGGCACAGAGATAGCCCTTGAAGGTGGAGCTCATTTGGTTGC 1080
Db 6694 CGTGTCACTTCTTAAACATGGAATCAAAGTATTACACTTCGCTCGGAACCTTTTGGCTGT 6753
Qy 1081 CAGATT 1086
Db 6754 GATATT 6759

Search completed: January 15, 2006, 19:27:31
Job time : 298 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 15:15:02 ; Search time 5449 Seconds
(without alignments)
12570.433 Million cell updates/sec

Title: US-10-813-588-1
Perfect score: 1464
Sequence: 1 atgacatctaagaattatcc.....caagtgatggcaggttaa 1464

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	869.2	59.4	1031	3	BM558496
2	741.8	50.7	839	6	CF785931
3	665	45.4	3600	4	CR749448
4	658.6	45.0	961	5	BU177739
5	652	44.5	652	7	CN404610
6	506	34.6	866	8	DN134443
7	489.6	33.4	913	6	CD109068
8	477.4	32.6	770	6	CB988462
9	451.4	30.8	1924	4	AK016485
10	451.4	30.8	2835	4	AK014521
11	445	30.4	956	5	BY713935
12	434.2	29.7	466	1	AW390343
13	427.4	29.2	683	5	EX360287
14	424.2	29.0	686	5	EX345014
15	405.4	27.7	798	6	CB960471
16	403.6	27.6	830	7	CN440576
17	394	26.9	736	8	CX755002
18	381.2	26.0	872	2	BG245910
19	356.8	24.4	404	11	DQ039380
20	355.4	24.3	434	1	AW483656
21	355.4	24.3	883	2	BG975603
22	352	24.0	404	11	DQ039381

23	351	24.0	790	6	CB959630
24	348.6	23.8	1150	3	BM805721
25	348	23.8	348	7	CN404612
26	347	23.7	802	6	CD110061
27	335.4	22.9	406	2	BF740455
28	335.2	22.9	478	10	CG521977
29	320.2	21.9	425	10	CZ293584
30	316.6	21.6	462	10	CL639277
31	312.8	21.4	600	5	BU924048
32	310.2	21.2	417	10	CZ293527
33	308.8	21.1	409	10	CZ293317
34	307	21.0	307	11	DQ046261
35	304.4	20.8	402	10	CZ293313
36	304.4	20.8	426	10	CZ293590
37	302	20.6	864	8	DR845229
38	294.2	20.1	745	5	BU449584
39	292.6	20.0	387	10	CG494608
40	290.2	19.8	509	10	CG636450
41	290.2	19.8	865	8	CX498307
42	289	19.7	456	10	CL302514
43	288	19.7	805	8	CX417452
44	285.2	19.5	388	10	CG662488
45	281.8	19.2	710	7	CN404614

ALIGNMENTS

RESULT 1
BM558496
LOCUS BM558496 1031 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT 6559394 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5741314
5' mRNA sequence.
ACCESSION BM558496
VERSION BM558496.1 GI:18801287
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1031)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12757 row: k column: 11
High quality sequence stop: 694.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5741314"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="NIH MGC 88"
/note="Organ: small intestine; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match

59.4%; Score 869.2; DB 3; Length 1031;

Best Local Similarity 95.9%; Pred. No. 9.5e-241; Matches 956; Conservative 0; Mismatches 34; Indels 7; Gaps 6;		CF785931		839 bp mRNA linear EST 20-OCT-2003	
QY		31		AGENCOURT_15989463 NIH_MGC_220 Homo sapiens cDNA clone	
Db		1		IMAGE:30707295 5', mRNA sequence.	
QY		91		AGTTGGGAGATTGGATATCGAATCCAGACCTGTGCTTCTGACTATCTTCTTCAC	
Db		61		AGTTGGGAGATTGGATATCGAATCCAGACCTGTGCTTCTGACTATCTTCTTCAC	
QY		151		AGCTCTTCAGATCAATATGCTCCATCTGGAAGTATGACTGTCCTCCAAAGCACTT	
Db		121		AGCTCTTCAGATCAATATGCTCCATCTGGAAGTATGACTGTCCTCCAAAGCACTT	
QY		211		TTGAACAACAGTGAAGTAAACCGTCTTTGAGAGTGGATCCCAATCTTCTGCGCGGGT	
Db		181		TTGAACAACAGTGAAGTAAACCGTCTTTGAGAGTGGATCCCAATCTTCTGCGCGGGT	
QY		271		TTTTTGTGCTGACCTATGCGAGCAGCCATCCAGATTTAATAATGTTTGGAAACGAGCT	
Db		241		TTTTTGTGCTGACCTATGCGAGCAGCCATCCAGATTTAATAATGTTTGGAAACGAGCT	
QY		331		AGCCATTTATTGAGACAGATACAGCAATCTGCGCAGCTGGTGTAGAGACGTAGCA	
Db		301		AGCCATTTATTGAGACAGATACAGCAATCTGCGCAGCTGGTGTAGAGACGTAGCA	
QY		391		GGAGACATTTCTGGGAATATGTTAGATGATATAGATACCTCTTTATTGTGCAAGCT	
Db		361		GGAGACATTTCTGGGAATATGTTAGATGATATAGATACCTCTTTATTGTGCAAGCT	
QY		451		GCCATCCATCCAGGAATTAATGCTGTGATGAACTAGGTGCGCAGATCACTGCTTCAGCGC	
Db		421		GCCATCCATCCAGGAATTAATGCTGTGATGAACTAGGTGCGCAGATCACTGCTTCAGCGC	
QY		511		AAGGGATCAGTCGATATGAAGGATTTCTGGCCATGCTGTTCTTTCGAGGGATGTTCC	
Db		481		AAGGGATCAGTCGATATGAAGGATTTCTGGCCATGCTGTTCTTTCGAGGGATGTTCC	
QY		571		CTGTCCAGCAAGCAGATTTCTGTTTACCTCAATGGTTCGACGAGATCCTTGAGTTTGA	
Db		541		CTGTCCAGCAAGCAGATTTCTGTTTACCTCAATGGTTCGACGAGATCCTTGAGTTTGA	
QY		631		CCTGACCGGCAAAATCAGAGCTTTCTTCATGCGAGTCGGTCAATGAGAGTGAGACCA	
Db		601		CCTGACCGGCAAAATCAGAGCTTTCTTCATGCGAGTCGGTCAATGAGAGTGAGACCA	
QY		691		GTTCACTGGTCTCTGCGCAAGCCGACTTCAGGACCAAGCCCATCATGGCTTCGGGC	
Db		661		GTTCACTGGTCTCTGCGCAAGCCGACTTCAGGACCAAGCCCATCATGGCTTCGGGC	
QY		751		GACAGTAGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA	
Db		721		GACAGTAGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA	
QY		810		GAAATAACAGGAATTAGGACCAAGATCTACAGTCGAACTTCACTTTTATG-TTA	
Db		781		GAAATAACAGGAATTAGGACCAAGATCTACAGTCGAACTTCACTTTTATG-TTA	
QY		869		AGAGTTTGTGATGAATCTTCAAAACCAATATCTTAAGTGAAGACCTATAAGGAATTG	
Db		841		AGAGTTTGTGATGAATCTTCAAAACCAATATCTTAAGTGAAGACCTATAAGGAATTG	
QY		929		TGAATAATGAAG--AAAAGTGTGTTTCAGGGTAACTCTAACTTTTC-GGACCCAGTGCAAA	
Db		899		TTGATATTGAAGAAAAGGGGTTTCAGGGTTAACTCTAACTTTTCGGGGACCAATTCGAA	
QY		986		ACAATTCATCCCTCCCATCGTGGCCAGATATGTGG 1022	
Db		959		AACATTTTCATCCCTCCCTCGTGGCCCNATAAATGTG 995	

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		/issue_type="prostate"	
		/clone_lib="686 (synonym: hlccc3). Vector pSport1_sfi; host DH10B; sites SfiIA + SfiIB"	
		/dev_stage="adult"	
		/note="hypothetical protein, N-terminus truncated, not fully spliced"	
gene		1..3600	
		/gene="DKFZp686L21135"	
CDS		-208..-5606	
		/gene="DKFZp686L21135"	
		/codon_start=1	
		/product="hypothetical protein"	
		/protein_id="CAH19285.1"	
		/db_xref="GI:51476606"	
		/translation="GDGCGHVTYODSGTMTSKNYPGTYPNHTVCEKTLTPKKGKELI LRLGLDIESQTCASDYLLFTSSSQOYGPYCSMTVPKELLINTSEVTVPFSGSHS GRGLITVASSDHPDLITCLERASHLYLKEFY"	
ORIGIN			
		Query Match 45.4%; Score 665; DB 4; Length 3600;	
		Best Local Similarity 91.1%; Pred. No. 3.2e-181;	
		Matches 748; Conservative 0; Mismatches 0; Indels 73; Gaps 1;	
QY	1	ATGACATCTAAGAATTTATCCCGGACCTACCCCAATCACACTGTTTTCGAAAGACAAT	60
DB	253	ATGACATCTAAGAATTTATCCCGGACCTACCCCAATCACACTGTTTTCGAAAGACAAT	312
QY	61	ACAGTACCAAGGGGAAAGACTGATCTGAGGTGGGAGATTGGATATCGAATCCCAG	120
DB	313	ACAGTACCAAGGGGAAAGACTGATCTGAGGTGGGAGATTGGATATCGAATCCCAG	372
QY	121	ACCTGTGCTTCTGACTATCTCTCTCACCAGCTCTTCAGATCAATATGTCCTCATACTGT	180
DB	373	ACCTGTGCTTCTGACTATCTCTCTCACCAGCTCTTCAGATCAATATGTCCTCATACTGT	432
QY	181	GGAGTATGACTGTTTCCCAAGAACTCTTGTGTGAACACAAAGTAAACCGTCCGCTTT	240
DB	433	GGAGTATGACTGTTTCCCAAGAACTCTTGTGTGAACACAAAGTAAACCGTCCGCTTT	492
QY	241	GAGAGTGGATCCCAATTTCTGCGCGGGGTTTTTGTGCTGACCTATCGGAGCGAGCCAT	300
DB	493	GAGAGTGGATCCCAATTTCTGCGCGGGGTTTTTGTGCTGACCTATCGGAGCGAGCCAT	552
QY	301	CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA	360
DB	553	CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAG	608
QY	361	TTCTGCCAGCTGTTGTAGACGCTAGCAGGAGACATTTTCTGGGAATATGGTAGTGA	420
DB	609	-----	608
QY	421	TATAGAGATACCTCTTTATTGTGCAAGCTGCCATCCATCGAGGAATAATTGCTGATGAA	480
DB	609	-----ACCTCTTTATTGTGCAAGCTGCCATCCATCGAGGAATAATTGCTGATGAA	659
QY	481	CTAGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATCAAGGGATTCTG	540
DB	660	CTAGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATCAAGGGATTCTG	719
QY	541	GCCAAATGGTGTCTTTTCGAGGGATGTTCCCTGTGTCAGACAGCGAATTTCTGTTTACCTCC	600
DB	720	GCCAAATGGTGTCTTTTCGAGGGATGTTCCCTGTGTCAGACAGCGAATTTCTGTTTACCTCC	779
QY	601	AATGTTGACAGAGATCTTGTGATTTTGAACCTGACGGGCAATTCAGAGCTTCTTCCTCA	660
DB	780	AATGTTGACAGAGATCTTGTGATTTTGAACCTGACGGGCAATTCAGAGCTTCTTCCTCA	839

QY 661 TGGCAGTCGTCATAGAGTGGAGACCAAGTTCACTGGTCTCTCTGGCCAGGCCGACTT 720
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 Db 840 TGGCAGTCGTCATAGAGTGGAGACCAAGTTCACTGGTCTCTCTGGCCAGGCCGACTT 899
 |||||
 QY 721 CAGGACCAAGGCCCATCATCGGCTTGGGGCGACAGTAGCAACCAACCAACCAACCAAGAG 780
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 Db 900 CAGGACCAAGGCCCATCATCGGCTTGGGGCGACAGTAGCAACCAACCAACCAACCAAGAG 959
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 QY 781 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAATAACAGG 821
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 Db 960 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAATAACAGG 1000
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RESULT 4
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 LOCUS
 DEFINITION AGENCOURT 7961999 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:6106770
 5', mRNA sequence.

ACCESSION BUI77739
 VERSION BUI77739.1 GI:22691723
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE
 1 (bases 1 to 961)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 DNA distribution: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHC2348 row: f column: 19
 High quality sequence stop: 591.

FEATURES
 source
 Location/Qualifiers

1..961
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6106770"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_39"
 /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAGAG(G). Library constructed
 by Ling Hong in the laboratory of Gerald M. Rubin
 (University of California, Berkeley) using ZAP-cDNA
 synthesis kit (Stratagene) and Superscript II RT (Life
 Technologies)."

ORIGIN
 Query Match 45.0%; Score 658.6; DB 5; Length 961;
 Best Local Similarity 98.0%; Pred. No. 1.6e-179;
 Matches 687; Conservative 0; Mismatches 11; Indels 3; Gaps 2;

QY 614 GATCCTTGAGTTTGAACCTGACGGGCAATCAGAGCTTCTCTCATGGCAGTCGGTCA 673
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Db 1 GATCCTTGAGTTTGAACCTGACGGGCAATCAGAGCTTCTCTCATGGCAGTCGGTCA 60
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QY 674 ATGAGATGGAGACCAAGTTCACTGGTCTCTGGCCAGGCCGACTTCAGGACCAAGGCC 733
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Db 61 ATGAGATGGAGACCAAGTTCACTGGTCTCTGGCCAGGCCGACTTCAGGACCAAGGCC 120
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QY 734 CATCATGGGCTTCGGGGCAGTAGCAACCAACCAACCAACCAACCAACCAACCAACCAAC 793
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Db 121 CATCATGGGCTTCGGGGCAGTAGCAACCAACCAACCAACCAACCAACCAACCAACCAAC 180
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 QY 794 ATTGGGGGAGAAAAGAAATTAACAGGAATTTAGGACCAACAGGATCTACACAGTCGAAC 853
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 Db 181 ATTGGGGGAGAAAAGAAATTAACAGGAATTTAGGACCAACAGGATCTACACAGTCGAAC 240
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 QY 854 TCAACTTTTATGTTAAGAGTTTGTGATGAATCTTCAAAAACAATAATTTCTAAGTGAAGA 913
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 Db 241 TCAACTTTTATGTTAAGAGTTTGTGATGAATCTTCAAAAACAATAATTTCTAAGTGAAGA 300
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 Db 301 CCTATAAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGTAATCTTAACTTTTCGGG 360
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 QY 974 ACCAGTGCAAAACAATTTTCACTCCCTCCCATCGTGCCAGATATGTGCGGGTTGTCCCC 1033
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 Db 361 ACCAGTGCAAAACAATTTTCACTCCCTCCCATCGTGCCAGATATGTGCGGGTTGTCCCC 420
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 QY 1034 AGACATGGCACCAAGAGTAGCTTGAAGGTGAGCTCATTTGGTTGCCAGATATACACAAG 1093
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 Db 421 AGACATGGCACCAAGAGTAGCTTGAAGGTGAGCTCATTTGGTTGCCAGATATACACAAG 480
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 QY 1094 GTAATGATTCATTGGTGTGCGGCAAGCAAGTCAAGAGCAGGAGTGTTCACACTTAAGAA 1153
 |||||
 Db 481 GTAATGATTCATTGGTGTGCGGCAAGCAAGTCAAGAGCAGGAGTGTTCACACTTAAGAA 540
 |||||
 QY 1154 AAGATGAGACAATCAACAGGCCCATCCCTCGGAAGAAATCCACA-GGAATAAACATT 1212
 |||||
 Db 541 AAGATGAGACAATCAACAGGCCCATCCCTCGGAAGAAATCCACAAGGAATAAACATT 600
 |||||
 QY 1213 ACAACGGTGGCTATTCCATTGGTGTCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1272
 |||||
 Db 601 ACAACGGTGGCTATTCCATTGGTGTCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 660
 |||||
 QY 1273 TTTTGACGCC--TTTACAAAGAGAGAAAGAAAGGAAGTCCG 1311
 |||||
 Db 661 TTTTGACGCCCTTTAGAAAGAAAGAAAGGAAGAAATTCG 701
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RESULT 5
 CN404610
 LOCUS 652 bp mRNA linear EST 16-MAY-2004
 DEFINITION 1700532579818 GRN_EB Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CN404610
 VERSION CN404610.1 GI:47392155
 KEYWORDS EST.

SOURCE
 Homo sapiens (human)

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE
 1 (bases 1 to 652)
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
 Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
 Lebkowski, J. and Stanton, L.W.

AUTHORS
 Transcription characterization elucidates signaling networks that
 control human ES cell growth and differentiation

TITLE
 Nat. Biotechnol. 22 (6), 707-716 (2004)

JOURNAL
 PUBMED 15146197

COMMENT
 Contact: Brandenberger R
 Regenerative Medicine
 Genon Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@genon.com

Insert Length: 652 Std Error: 0.00.
 Location/Qualifiers
 1..652
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"

FEATURES
 source

/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_lib="GRN EB"
/note="oligo dt primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

ORIGIN

Query Match 44.5%; Score 652; DB 7; Length 652;
Best Local Similarity 100.0%; Pred. No. 1.2e-177; Indels 0; Gaps 0;
Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 358 AAATCTGCCCAGCTGTTGTAGACAGCTAGCAGGAGACATTTCTGGGAATATGTTAGAT 417
DB 1 AAATCTGCCCAGCTGTTGTAGACAGCTAGCAGGAGACATTTCTGGGAATATGTTAGAT 60
QY 418 GGATATAGAGATACCTCTTTATTTGTGCAAGCTGCCATCATCAGAGAAATATGTTGAT 477
DB 61 GGATATAGAGATACCTCTTTATTTGTGCAAGCTGCCATCATCAGAGAAATATGTTGAT 120
QY 478 GAACTAGGTGGCCAGATCAGTGTCTTCAGCGCAAGAGGATCAGTCGATATGAAGGAT 537
DB 121 GAACTAGGTGGCCAGATCAGTGTCTTCAGCGCAAGAGGATCAGTCGATATGAAGGAT 180
QY 538 CTGGCCAAATGTTGTTCTTTCGAGGGATGTTCTCCTGTGACACAAGCGATTTCTGTTTACC 597
DB 181 CTGGCCAAATGTTGTTCTTTCGAGGGATGTTCTCCTGTGACACAAGCGATTTCTGTTTACC 240
QY 598 TCAATGTTGACAGAGATCCTTTAGTTTGAACCTTGACGGGCAAAATCAGAGCTTCTTCC 657
DB 241 TCAATGTTGACAGAGATCCTTTAGTTTGAACCTTGACGGGCAAAATCAGAGCTTCTTCC 300
QY 658 TCATGCGAGTCCGTCAATGAGTGGAGACCAAGTTTCACTGTTCTCTCGCCCAAGCCGA 717
DB 301 TCATGCGAGTCCGTCAATGAGTGGAGACCAAGTTTCACTGTTCTCTCGCCCAAGCCGA 360
QY 718 CTTTACAGCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACAACCAACCAACCA 777
DB 361 CTTTACAGCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACAACCAACCAACCA 420
QY 778 GAGTGGCTGGAGATCGATTTGGGGAGAAAAAGAAATACAGGAATTAGGACCAACAGA 837
DB 421 GAGTGGCTGGAGATCGATTTGGGGAGAAAAAGAAATACAGGAATTAGGACCAACAGA 480
QY 838 TCTACACACTCGAATCTCACTTTTATGTTTATGAGTGTGATGAACTTCAAAACAT 897
DB 481 TCTACACACTCGAATCTCACTTTTATGTTTATGAGTGTGATGAACTTCAAAACAT 540
QY 898 AATTCTTAAGTGAAGACCTATAAGGAATTTGTAATTAATGAAGAAAGGTGTTTCAAGGT 957
DB 541 AATTCTTAAGTGAAGACCTATAAGGAATTTGTAATTAATGAAGAAAGGTGTTTCAAGGT 600
QY 958 AACTCTAACTTTTCGGGACCCAGTGCAGAAACAAATTTTCATCCCTCCCATCGTG 1009
DB 601 AACTCTAACTTTTCGGGACCCAGTGCAGAAACAAATTTTCATCCCTCCCATCGTG 652

RESULT 6

DNI34443
LOCUS 866 bp mRNA linear EST 15-FEB-2005
DEFINITION 996566 MARC 4P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION DNI34443
VERSION DNI34443.1 GI:59828760
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus
1 (bases 1 to 866)
REFERENCE Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
Nonneman,D.J., Wray,J.E. and Keele,J.W.

TITLE
JOURNAL
COMMENT

Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: TMW8069 row: N column: 5
Seq primer: GTAATACGACTCCTATAGG.
Location/Qualifiers
1..866
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/issue_type="pooled"
/lab_host="DH108"
/clone_lib="MARC 4P1G"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."

FEATURES
source

Query Match 34.6%; Score 506; DB 8; Length 866;
Best Local Similarity 84.5%; Pred. No. 3.5e-135;
Matches 598; Conservative 0; Mismatches 95; Indels 15; Gaps 2;
QY 768 CAAACACAGAGTGGCTGGAGATCGATTTGGGGAGAAAAAGAAATAACAGGAATTAG 827
DB 9 CAAACAGAGAGTGGCTGGAGATCGATTTGGGGAGAAAAAGAAATAACAGGAATTAG 68
QY 828 GACCAAGAGATCTACAGTCCAACTTTTATGTTTAAAGAGTTTGTGATGAACCT 887
DB 69 GACCAAGAGATCCACAGTCAAAATTTCACTTTTACGTAAAGAGTTTGTGTAAGAACT 128
QY 888 CAAAACATATTTCTAAGTGAAGACCTATAAGGAATTTGTAATTAAGGAAGAGT 947
DB 129 CAAAGCAATAGTCCAAAGTGAAGACTTTATAAGGAATTTGGGAATTAATGAAGAAAGT 188
QY 948 GTTTCAGGGTAACTCTAACTTTTCGGGACCCAGTGCAGAAACAAATTTTCATCCCTCCCATCGT 1007
DB 189 GTTTCAGGCACTCTAATTTTCGGGATCCCGTGGGAACAACCTTCCTCCCATTTGT 248
QY 1008 GGCAGAGATATGCGGGTGTCTCCCAACATGACATGGCAACAGAGATAGCCTTGAAGTGA 1067
DB 249 GGCAGAGATACATACGCTTATCCCCATACCTGGCACAGAGATAGCCTTGAAGTGA 308
QY 1068 GCTCATTTGTTGCCAGATTACA-----CAGGTAATGATTCATTTGTTGGGCG 1115
DB 309 GCTTCTGGCTGCCAGATTACACCAAGTAGGACTCAGGGTAATGACTCATTTGGTGTGGCC 368
QY 1116 CAAAGCAAGTCAAAAGCAGCAGTGTTCACCTAAGAAAGAGATGACACATCAAGAGCC 1175
DB 369 CAGAACAGTTCAATATCTGTTGGCTCAACTAAAGAGAGATGAGCAATCTCAACACC 428
QY 1176 CATCCCTCGGAAGAAACATCCACAGGAATAACATATACACGGTGGCTATTTCATTGTT 1235
DB 429 CATCCCTCTGAAGAAATGACCAAGAGATTAAACATCACAACCTGTTGTTTATTCCTCGGT 488
QY 1236 GCTCCTGTTGCTGGTGTGTTGCTGGAATGGGATCTTTGACGCCCTTTAGAAAGAGAA 1295
DB 489 GCTCC---TCGCCCTGCTGATTGCTGGAGTGGAACTTTTGCATCTTTAGAAAGAGAA 545
QY 1296 GAAAGAAAGAGTCCGTATGAGTACGCGGAGCTCAGAAAAACAGACTGTTGGAAGCAGAT 1355
DB 546 GAAAGAAAGAGTCCGTATGAGTACGCTAAGACTCAGAAAAACAGATTGTTGGAAGCAGAT 605
QY 1356 TAAATATCCCTTTGCCAGACATCAGTCACTGAGTTTACCATCAGCTATGATAATGAGAA 1415

Db 606 CAAATATCCCTTGGCCAGGATCAGTCAGTGAAGTTTACCATCAGTCAGTCAGTCAATGAAAA 665

QY 1416 GGAGATGACACAAAAGTTAGATCTCATCAAGTGTATGGCAGGTTA 1463

Db 666 GGAGATGACACAAAAGTTGGATCTCATCAAGTGTATGGCAGGTTA 713

RESULT 7
CD109068 913 bp mRNA linear EST 15-MAY-2003
LOCUS AGENCOURT 14020178 NIH_MGC_179 Homo sapiens cDNA clone
DEFINITION IMAGE:30367004 5', mRNA sequence.

ACCESSION CD109068
VERSION CD109068.1 GI:30762242
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 913)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM427 row: h column: 21
High quality sequence start: 15
High quality sequence stop: 652.
Location/Qualifiers

FEATURES
source
1. 913
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30367004"
/tissue_type="Pituitary"
/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/clone_lib="NIH_MGC_179"
/notes="Organ: brain; Vector: pCMV-SPORT6.1; Site 1: EcoRV
(destroyed); Site 2: NotI; Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.1 kb. Library was
constructed by (Invitrogen). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 33.4%; Score 489.6; DB 6; Length 913;
Best Local Similarity 95.5%; Pred. No. 2.1e-130;
Matches 569; Conservative 0; Mismatches 19; Indels 8; Gaps 6;
QY 1 ATGACATCTAAGAAATTATCCGGGACCTACCCCAATCACACTGTTTCGGAAGACAAATT 60
Db 299 ATGACATCTAAGAAATTATCCGGGACCTACCCCAATCACACTGTTTCGGAAGACAAATT 358
QY 61 ACAGTACCAAGGGGAAAGACTGATTTCTGAGGTTGGGAGATTGGATATCGAATCCAG 120
Db 359 ACAGTACCAAGGGGAAAGACTGATTTCTGAGGTTGGGAGATTGGATATCGAATCCAG 418
QY 121 ACCTGTGCTTGTGACTCTCTCTTCCACAGCTCTTCAGATCAATATGTCATATCTGT 180
Db 419 ACCTGTGCTTGTGACTCTCTCTTCCACAGCTCTTCAGATCAATATGTCATATCTGT 478
QY 181 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTGAACCAAGTGAAGTAAACCGTCCGCTTT 240
Db 479 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTGAACCAAGTGAAGTAAACCGTCCGCTTT 538

QY 241 GAGAGTGGATCCACATTTCTGGCCGGGGTTTTTGTGCTGACCTATGCGAGCAGCCACAT 300

Db 539 GAGAGTGGATCCACATTTCTGGCCGGGGTTTTTGTGCTGACCTATGCGAGCAGCCACAT 598

QY 301 CCAGATTTTAAATAACATGTTTGGAAAGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA 360

Db 599 CCAGATTTTAAATAACATGTTTGGAAAGAGCTAGCCATTATTTGAAGACAGAAATACAGCAA 658

QY 361 TTCTGCCACAGCTGTTGTAGACAGCTAGCA - GGAGACATTTCTGGGAATATGTTAGATGG 419

Db 659 TTCTGCCACAGCTGTTGTAGACAGCTAGCAAGGAGACATTTCTGGGAATATGTTAGATGG 718

QY 420 ATATAGAGATACCTCTTTATTTGTGCAAGCTGCCATCCATGCGAGGATTAATTG - CTGATG 478

Db 719 ATATAGAGATACCTCTTTATTTGTGCAAGCTGCCATCCATGCGAGGATTAATTGCTGATG 778

QY 479 AACTA - GTGTGGCCAGATCAGT - GTGCTTCAGCGCAAGAGGATCAGTCGATATGAAGGGAT 536

Db 779 AACTANGTGGCCAGATCATTGTTGCTTCGCCGCAAGAGATCAGTCATATGAAGGGAT 838

QY 537 TCTGGCCAAATGG - TGTTCTTTTCGAGGATGG - TTCCCTGTCCAGCAAGCGGATTT 588

Db 839 TCTGGCCAAAGGTGGTCTCTTCAAGGGAAGGGTTCCTCTGGTCAAAACAAGCGAATT 894

RESULT 8
CB988462 770 bp mRNA linear EST 01-MAY-2003
LOCUS AGENCOURT 13903537 NIH_MGC_147 Homo sapiens cDNA clone
DEFINITION IMAGE:30342255 5', mRNA sequence.

ACCESSION CB988462
VERSION CB988462.1 GI:30282982
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 770)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM375 row: a column: 16
High quality sequence stop: 607.
Location/Qualifiers

FEATURES
source
1. 770
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30342255"
/tissue_type="Human Placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_147"
/notes="Organ: placenta;
all-XhoI; Site 2: BamHI; Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: This is
a NIH_MGC library."

ORIGIN

with BamHI and XhoI. cDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

FEATURES

source

Location/Qualifiers

1..2835
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="FANTOM DB:4631413K11"
 /db_xref="taxon:10090"
 /clone="4631413K11"
 /tissue_type="skin"
 /dev_stage="0 day neonate"
 74..1456
 /note="unnamed protein product; hypothetical LCCL domain/CUB domain containing protein (InterPro|IPR004043, InterPro|IPR000859, evidence: InterPro) putative"

CDS

74..1456
 /note="unnamed protein product; hypothetical LCCL domain/CUB domain containing protein (InterPro|IPR004043, InterPro|IPR000859, evidence: InterPro) putative"

/codon_start=1

/protein_id="BAB29409.1"

/db_xref="GI:12852431"

/translation="MTSKNYPGYPNYTVCKEIIIVPKGRILRLDNLIESKTCAS
 DYLLFSATDQPGYCGSWAPKELRLNNEVTLFKSGSHISGRFLITLTYSSDHPD
 LITCLERGHYFEKYSKFCPCAGRDIAIGNTKQYRDTSLICKAAIHAGIITDE
 LGHINLLOSKEGISHYGLANGVLNRHGLSLKRLFTTPGWNITVAIPSVIRIATL
 LITGMGIFAICRKKKNGPNYSADAQKQKQIKYFPAHQSTEFITSYNEKEMT
 QKDLITSDMADYQQPLMTGTIVARKSTFRFMDTDEVRNTEASGHYDCPHRPG
 RHYALPLTHPEYATPIVERHLLRAHTFSTQGYRVPFRPHKHSYSGGFFPAT
 GATQVESYQRPAKPVPVGGYDKPAASSFLDSRPSQSQTSGGDDGYSAFNRGLAP
 LMQNTALL"

2816..2821

/note="putative"

polya_signal

2835

/note="putative"

ORIGIN

Query Match 30.8%; Score 451.4; DB 4; Length 2835;
 Best Local Similarity 84.1%; Pred. No. 3.7e-119;
 Matches 509; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 1 ATGACATCTAAGAATTATCCCGGAGCTACCCCAATCACACTGTTTTCGGAAGAACAAT 60
 DB 74 ATGACATCTAAGAATTATCAGGAGCTTACCCCAATTACACTGTGTGGAAGAATCATC 133
 QY 61 ACAGTACCAAGGGGAAAGACTGATCTGAGTTGGAGATTGGATATCGAATCCAG 120
 DB 134 ACAGTCCCAAGGGGAAAGACTTATCTGAGTTGGAGATTGGAACATTTGAGTCCAAAG 193
 QY 121 ACCGTGCTTCTGACTATCTCTTCCACCAGCTCTTCAGATCAATATGTCCTACTGT 180
 DB 194 ACCTGCGCTTCTGACTATCTCTTCCAGGATGCAACAGATCAGTATGTCCTATGTT 253
 QY 181 GGAAGTATGACTGTTTCCCAAGAACTCTTGTGGAACACAAAGTGAAGTACCGTCCGCTTT 240
 DB 254 GCGAGTTGGCTGTTCCCAAGAACTCCCGTGAACCTCAACAGAGTACTGTCTCTTC 313
 QY 241 GAGAGTGAATCCACATTTCTGCGCGGGTTTTTCTGCTACCTATCGGAGCGAGCCAT 300
 DB 314 AAGAGTGAATCTCACATTTCTGCGCGGGCTTTCTGCTGACCTACCCAGCAGTGAACAT 373
 QY 301 CCAGATTTAATACATGTTTGAACACGAGTACGCATTATTTGAAGACAGAAATACACAAA 360
 DB 374 CCAGATTTAATACCTGTTTGGACGAGCAGCCATTATTTGAGGAAATAATACACAAA 433
 QY 361 TTCTGCCAGCTGGTTGTAGACAGTGTAGCAGGAGACATTTCTGGGAATATGTTAGATGA 420
 DB 434 TTCTGCCAGCTGGTTGTAGACATAGCAGGAGATTTCTGGGAATACAAAAGTGT 493
 QY 421 TATAGAGATACCTCTTTTATTTGCAAGCTGCCATCCATCGAGGAATAATATGCTGATGA 480
 DB 494 TACAGAGATACCTCTTTTATTTGTGCAAGCTGCCATCCAGCGAGGATCATCAGATGAA 553

QY 481 CTAGTGGCCAGATCAGTGTCTTTCAGCGAAGGATCAGTCGATATGAAGGATCTCTG 540
 DB 554 CTAGTGGCCAGATCAGTGTCTTTCAGCGAAGGATCAGTCGATATGAAGGATCTCTG 613
 QY 541 GCCAATGGGTGTTCTTTTCGAGGGATGTTCCCTCTCAGACAAGGATTTCTGTGTACCTCC 600
 DB 614 GCCAATGGGTGTTCTTTTCGAGGGATGTTCTTTTCGGAAGGATTTCTTTTACCAAC 673
 QY 601 AATGG 605
 DB 674 CCAGG 678

RESULT 11

BY713935

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

BY713935 956 bp mRNA linear EST 17-DEC-2002
 BY713935 RIKEN full-length enriched, 0 day neonate skin Mus
 musculus cDNA clone 4631413K11 5', mRNA sequence.

BY713935 GI:27126105

EST.

Mus musculus (house mouse)

Mus musculus

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 956)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaido, I., Oato, N., Saito, R., Suzuki, H., Yamanaka, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
 Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
 Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Bruscia, V.,
 Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,
 Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmer, S.,
 Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
 Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
 Kurochkin, I. V., Lee, X., Lenhard, B., Lyons, P. A., Maglott, D. R.,
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
 Numata, K., Okido, T., Pavan, W. J., Perte, G., Pesole, G.,
 Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
 Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
 Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,
 Sulcano, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
 Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
 Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
 Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
 Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

12466851

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,

Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,

Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,

Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,

Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,

Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,

Takeda, Y., Waki, K., Watabiki, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in Riken,
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.
 Location/Qualifiers
 1. .956
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="4631413K11"
 /sex="mixed"
 /tissue_type="skin"
 /dev_stage="0 day neonate"
 /lab_host="DH108"
 /clone_lib="RIKEN full-length enriched, 0 day neonate
 skin"
 /notes="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 10.0 and subtraction to Rot = 100.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5' GAGAGAGATCTCGAGTTAATTAATTAATCCCCCCCC
 3']. cDNA was cloned into the XhoI and BamHI sites.
 Vector: a modified pBluescript KS(+) after bulk excision
 from Lambda FLX I"

ORIGIN

Query Match 30.4%; Score 445; DB 5; Length 956;
 Best Local Similarity 83.5%; Pred. No. 2e-117;
 Matches 505; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
 Qy 1 ATGACATCTAAGATTATCCGGGACCTACCCCAATCACACTGTTTGGGAAAGACAATT 60
 Db 69 ATGACATCTAAGATTATCCAGGACCTTACCCCAATTACACTGTGTGTTGAAAGATCATC 128
 Qy 61 ACAGTACAAAGGGGAAAGACTGATCTTGAGTTGGAGATTGGATATCGAATCCAG 120
 Db 129 ACAGTCCAAAGGGGAAAGAGACTTATCTGAGTTGGAGATTGGAACATTTGAGTCCAAAG 188
 Qy 121 ACCGTGCTCTGACTATCTCTCTTCCACAGCTCTTCAGATCAATATGGTCCACTATGT 180
 Db 189 ACCGTGCTCTGACTATCTCTCTTTCAGAGTGAACAGATCAGTATGTCATATGT 248
 Qy 181 GGAAAGTATGACTGTTCCCAAGAACTCTTGTGAAACAAGTGAAGTAACCGTCCGCTTT 240
 Db 249 GGGAGTTGGGCTGTTCCCAAGAACTCCGGCTGAACCTCAAACGAGTGAAGTCTCTCTTC 308
 Qy 241 GAGAGTGGATCCCACTTTCTGGCGGGGGTTTTTGTGCTATGAGCTATGGAGCGGACCAT 300

Db 309 AAGAGTGGATCTCACATTTCTGGCGGGGCTTTCTGTGACCTAGCCAGCAGTGACCAT 368
 Qy 301 CCAGATTTTAATAACATGTTTGGAAAGAGCTAGCCATTAATTTGAAGACAGAATACAGCAA 360
 Db 369 CCAGATTTTAATAACCTGTTTGGAAAGAGCGGAGCCATTAATTTGAGGAAAAATACAGCAA 428
 Qy 361 TTCTGCCAGCTGGTGTAGAGACGTAGCAGGAGACATTTCTGGGGAATATGGTAGATGA 420
 Db 429 TTCTGCCAGCTGGCTGTAGAGACATAGCAGGAGATTAATTTCTGGGAATACAAAAGATGGT 488
 Qy 421 TATAGAGATACCTCTTTATTTGCAAGCTGCCATCCATGCGAGGATATTTCTGTATGA 480
 Db 489 TACAGAGATACCTCTTTATTTGTGCAAGCTGCCATCCAGCAGGGGATCATACAGATGA 548
 Qy 481 CTAGGTGGCGAGATCAGTGTCTTTCAGCCGCAAGGATCAGTCGATATGAAGGATTTCTG 540
 Db 549 CTAGGTGGCGACATCACTTGTCTTTCAGAGCAAGGATTAAGTCACTATAGAGGACTCTG 608
 Qy 541 GCAATGGTGTCTTTCTGAGGAGATGTTCCCTGTCAGACAGGATTTCTGTTTACTCTCC 600
 Db 609 GTCAATGGGCTGCTCTCCCGCATGTTCTTTGTGCGAAGAGCGATTTCTTTTACAACC 668
 Qy 601 AATGG 605
 Db 669 CCAGG 673
 RESULT 12
 AM390343/C
 LOCUS
 DEFINITION RC4-ST0185-131099-011-c01 ST0185 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AM390343
 VERSION AM390343.1 GI:6895002
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 REFERENCE 1 (bases 1 to 466)
 HGCP <http://www.ludwig.org.br/ORESTES>.
 AUTHORS The FAPESP/LICR Human Cancer Genome Project
 TITLE Unpublished (1999)
 JOURNAL Contact: Simpson A.J.G.
 COMMENT Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC4&t2=RC4-ST0185-131099-011-c01&t3=1999-10-13&t4=i>)
 Seq primer: puc 18 forward
 High quality sequence start: 26
 High quality sequence stop: 204.
 FEATURES
 Location/Qualifiers
 1. .466
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="ST0185"
 /note="Organ: stomach; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

```
Query Match      29.7%; Score 434.2; DB 1; Length 466;
Best Local Similarity 97.0%; Pred. No. 2.2e-114;
Matches 453; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

QY 512 AAGGATCATGTCGATATGAAGGATCTTGCCCAATGGTGTCTTTTCGAGGATGTTGCC 571
DB 466 AAGGATCATGTCGATATGAAGGATCTTGCCCAATGGTGTCTTTTCGAGGATGTTGCC 407

QY 572 TGTTCACAGAGGATCTTGTGTACCTCCATGCTTGCCAGCATCTTGAGTTTGAAC 631
DB 406 TGTTCACAGAGGATCTTGTGTACCTCCATGCTTGCCAGCATCTTGAGTTTGAAC 347

QY 632 CTGACGGGCAAAATCAGAGCTTCTTCTCATGCGAGTCGGTCAATGAGAGTGGAGACCAAG 691
DB 346 CTGACGGGCAAAATCAGAGCTTCTTCTCTTGGCAGTCGGTCAATGAGTGGAGACCAAG 287

QY 692 TTCACCTGCTCTCTGCCCAGCCGACTTCAGGACCAAGGCCCATCATGGCTTCGGGCG 751
DB 286 TTCACCTGCTCTCTGCCCAGCCGACTTCAGGACCAAGGCCCATCATGGCTTCGGGCG 227

QY 752 ACAGTAGCACACACCAACCAACGAGAGTGGCTGAGATCGATTTGGGGGAGAAAAAGA 811
DB 226 ACAGTAGCACACACCAACCAACGAGAGTGGCTGAGATCGATTTGGGGGAGAAAAAGA 167

QY 812 AAATAACAGGAATTTAGGACACACAGGATCTACACAGTCGAACCTTCAACTTTTATGTTAAGA 871
DB 166 AAATAACAGGAATTTAGGACACACAGGATTTTACACAGTCGAACCTTCAACTTTTATGTTAAGA 107

QY 872 GTTTTGTGATGAATTTCAAAAAACAATTAATTTAAAGTGGAGACCTATAAGGAATTTGTA 931
DB 106 GTTTTGTGATGAATTTCAAAAAACAATTAATTTAAAGTGGAGACCTATAAGGAATTTGTA 47

QY 932 ATAATGAAGAAAGGTTTTCAGGTTAACTTCAACTTTTCGGGACCCA 978
DB 46 ATAATGAAGAAAGGTTTTCAGGTTAACTTCAACTTTTCGGGACCCA 1
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RESULT 13

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BX360287
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
```

BX360287 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI067YN20 5-PRIME, mRNA sequence.
BX360287
BX360287.2 GI:46306639
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 683)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30376427.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3863.f

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?cna=CS0DI067YN20&id=3863.f>.
Location/Qualifiers
1. .683
/organism="Homo sapiens"
/mol_type="mRNA"

FEATURES
source

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/db_xref="taxon:9606"  
/clone="CS0DI067YN20"  
/tissue_type="PLACENTA COT 25-NORMALIZED"  
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with NotI and cloned into the NotI and EcoRV  
sites of the pCMVSPORT 6 vector. Library was normalized."
```

ORIGIN

Query Match 29.2%; Score 427.4; DB 5; Length 683;
Best Local Similarity 99.8%; Pred. No. 2.3e-112;
Matches 428; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTCTTTTCGGAAGACAATT 60
DB 255 ATGACATCTAAGAAATTTATCCCGGACCTACCCCAATCACACTCTTTTCGGAAGACAATT 314

QY 61 ACAGTACCAAAAGGGGAAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCCAG 120
DB 315 ACAGTACCAAAAGGGGAAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCCAG 374

QY 121 ACTGTGCTTCTGACATCTTCTTCCACAGCTCTTCAGATCAATATGTTCCATCTGT 180
DB 375 ACTGTGCTTCTGACATCTTCTTCCACAGCTCTTCAGATCAATATGTTCCATCTGT 434

QY 181 GGAAGTATGACCTGTTCCCAAGAACTCTTTGTTGAACACAAAGTAAACCGTCCGCTTT 240
DB 435 GGAAGTATGACCTGTTCCCAAGAACTCTTTGTTGAACACAAAGTAAACCGTCCGCTTT 494

QY 241 GAGAGTGGATCCCAATTTCTGCGCGGGGTTTTTGTCTGACCTATTCGAGCAGCGACCAT 300
DB 495 GAGAGTGGATCCCAATTTCTGCGCGGGGTTTTTGTCTGACCTATTCGAGCAGCGACCAT 554

QY 301 CCAGATTTAATAACATGTTTGGAAACAGCTAGCCATTTTGAAGACAGATAACAGCAA 360
DB 555 CCAGATTTAATAACATGTTTGGAAACAGCTAGCCATTTTGAAGACAGATAACAGCAA 614

QY 361 TTCTGCCAGCTGTTGTAGACAGCTAGCAGAGACATTTCTGGGAATATGGTAGTGA 420
DB 615 TTCTGCCAGCTGTTGTAGACAGCTAGCAGAGACATTTCTGGGAATATGGTAGTGA 674

QY 421 TATAGAGAT 429
DB 675 TATAGAGAT 683

RESULT 14
BX345014
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BX345014 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI067YN20 5-PRIME, mRNA sequence.
BX345014
BX345014.2 GI:46279671
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 686)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 2, 2003 this sequence version replaced gi:30342328.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3863.f

division of Invitrogen. This sequence belongs to sequence cluster 3863.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?se=CS2BAX14ZH08_AX24ZE2_1&c=3863.f.

FEATURES

source
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CS001067Y20"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 29.0%; Score 424.2; DB 5; Length 686;
Best Local Similarity 99.3%; Pred. No. 2e-111;
Matches 426; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACACTCTTTGCGAAAGACAATT 60
DB 258 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACACTCTTTGCGAAAGACAATT 317
QY 61 ACAGTACCAAGGGGAAAGACTGATCTGAGGTTGGAGATTTGGATATCGAATCCCGAG 120
DB 318 ACAGTACCAAGGGGAAAGACTGATCTGAGGTTGGAGATTTGGATATCGAATCCCGAG 377
QY 121 ACTGTGCTTCTGACTATCTCTTCCACAGCTCTTCAGATCAATATGTCATCTATGTT 180
DB 378 ACTGTGCTTCTGACTATCTCTTCCACAGCTCTTCAGATCAATATGTCATCTATGTT 437
QY 181 GGAAGTATGACTGTTCCCAAGAACTCTTGTGAACACAAGTGAAGTAAACCGTCCGCTTT 240
DB 438 GGAAGTATGACTGTTCCCAAGAACTCTTGTGAACACAAGTGAAGTAAACCGTCCGCTTT 497
QY 241 GAGAGTGGATCCCAATCTTCTGCGCGGGGTTTTTGTGACCTATGCGAGCAGGACCAT 300
DB 498 GAGAGTGGATCCCAATCTTCTGCGCGAGGTTTTTGTGACCTATGCGAGCAGGACCAT 557
QY 301 CCAGATTAAATACATGTTTGGAAAGAGTAGCCATTTATTTGAAGACAGAAATACAGAAA 360
DB 558 CCAGATTAAATACATGTTTGGAAAGAGTAGCCATTTATTTGAAGACAGAAATACAGAAA 617
QY 361 TTCTGCCCGAGCTGTTGAGAGAGTAGCAGGAGACATTTCTGGGAATATGTTAGATGGA 420
DB 618 TTCTGCCCGAGCTGTTGAGAGAGTAGCAGGAGACATTTCTGGGAATATGTTAGATGGA 677
QY 421 TATAGAGAT 429
DB 678 TATAGAGAT 686

RESULT 15

CB960471
LOCUS CB960471 798 bp mRNA linear EST 29-APR-2003
DEFINITION AGENCOURT 13887572 NIH MGC_147 Homo sapiens cDNA clone
IMAGE:30347405 5', mRNA sequence.

ACCSSION CB960471

VERSION CB960471.1 GI:30216587

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 798)

NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDAM388 row: h column: 06
High quality sequence stop: 707.

FEATURES

source
1. .798
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30347405"
/issue_type="Human Placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC_147"
/note="Organ: placenta; Vector: pBluescriptR; Site 1:
all-XhoI; Site 2: BamH; Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: This is
a NIH_MGC library."

ORIGIN

Query Match 27.7%; Score 405.4; DB 6; Length 798;
Best Local Similarity 99.8%; Pred. No. 6e-106;
Matches 406; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACACTCTTTGCGAAAGACAATT 60
DB 363 ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACACTCTTTGCGAAAGACAATT 422
QY 61 ACAGTACCAAGGGGAAAGACTGATTTCTGAGGTTGGAGATTTGGATATCGAATCCCGAG 120
DB 423 ACAGTACCAAGGGGAAAGACTGATTTCTGAGGTTGGAGATTTGGATATCGAATCCCGAG 482
QY 121 ACCTGTGCTTCTGACTATCTCTTCCACAGCTCTTCAGATCAATATGTCATCTATGTT 180
DB 483 ACCTGTGCTTCTGACTATCTCTTCCACAGCTCTTCAGATCAATATGTCATCTATGTT 542
QY 181 GGAAGTATGACTGTTCCCAAGAACTCTTGTGAACACAAGTGAAGTAAACCGTCCGCTTT 240
DB 543 GGAAGTATGACTGTTCCCAAGAACTCTTGTGAACACAAGTGAAGTAAACCGTCCGCTTT 602
QY 241 GAGAGTGGATCCCAATTTCTGCGCGGGGTTTTTGTGACCTATGCGAGCAGGACCAT 300
DB 603 GAGAGTGGATCCCAATTTCTGCGCGGGGTTTTTGTGACCTATGCGAGCAGGACCAT 662
QY 301 CCAGATTAAATACATGTTTGGAAAGAGTAGCCATTTATTTGAAGACAGAAATACAGAAA 360
DB 663 CCAGATTAAATACATGTTTGGAAAGAGTAGCCATTTATTTGAAGACAGAAATACAGAAA 722
QY 361 TTCTGCCCGAGCTGTTGAGAGAGTAGCAGGAGACATTTCTGGGAA 407
DB 723 TTCTGCCCGAGCTGTTGAGAGAGTAGCAGGAGACATTTCTGGGGA 769

Search completed: January 15, 2006, 19:22:26

Job time : 5454 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 15, 2006, 14:09:37 ; Search time 864 Seconds

(without alignments)
11292.951 Million cell updates/sec

Title: US-10-813-588-1

Perfect score: 1464

Sequence: 1 atgacatctaagaattatcc.....caagtgatatgcaggttaa 1464

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1464	100.0	1620	4 AAS00615	Aas00615 Novel hum
2	1464	100.0	1761	4 AAS00614	Aas00614 Novel hum
3	1464	100.0	1768	4 AAS00613	Aas00613 Novel hum
4	1462.4	99.9	1761	11 ADN39765	Adn39765 Cancer/an
5	1462.4	99.9	2010	11 ADN39764	Adn39764 Cancer/an
6	1462.4	99.9	2010	13 ADR46610	Adr46610 Cancer-as
7	1462.4	99.9	2010	13 ADR46611	Adr46611 Cancer-as
8	1459.8	99.7	2145	8 ACD66718	Ac66718 Secreted
9	1459.8	99.7	2145	12 ADQ10135	Adq10135 Human pol
10	1459.8	99.7	2888	6 ADI28055	Adi28055 ECMCAD ge
11	1459.8	99.7	3591	6 ABN86493	Abn86493 Human neu
12	1459.8	99.7	3594	4 AAS00660	Aas00660 Human TAN
13	1459.8	99.7	3594	8 ACD66717	Ac66717 Secreted
14	1459.8	99.7	3594	12 ADQ10134	Adq10134 Human pol
15	1459.8	99.7	3676	5 ADL62155	Adl62155 Human ova
16	1440.2	98.4	2547	11 ADM02314	Adm02314 Human CDN
17	1107.4	75.6	2310	11 ADN39766	Adn39766 Cancer/an
18	1040.6	71.1	2145	6 ABN86496	Abn86496 Human zcu
19	584.2	39.9	2473	11 ADM03690	Adm03690 Human CDN

20	584.2	39.9	2473	14 ADV18582	Adv18582 DNA encod
21	565.6	38.6	636	8 ACA10146	ACA10146 Human NOV
22	564.2	38.5	1538	8 ACA10145	ACA10145 Human NOV
23	564.2	38.5	1538	12 ADO08322	ADO08322 Human NOV
24	563	38.5	636	12 ADO08324	ADO08324 Human NOV
25	556	38.0	1265	6 AAD35992	Aad35992 Human neu
26	556	38.0	1265	6 ABK49565	Abk49565 Human CDN
27	556	38.0	1265	10 ADC29936	Adc29936 Human nov
28	548	37.4	596	14 ADV74982	Adv74982 Human col
29	451.4	30.8	2836	6 ABN86494	Abn86494 Mouse zcu
30	449.8	30.7	1871	3 AAA96736	Aaa96736 Polynucle
31	414.4	28.3	456	9 ACH31919	Ach31919 Human end
32	400	27.3	400	14 ADV74981	Adv74981 Human col
33	368.2	25.2	1509	6 ABN86497	Abn86497 Mouse zcu
34	223	15.2	2868	6 ABN86495	Abn86495 Mouse zcu
35	219.4	15.0	407	2 AAV87469	Aav87469 EST clone
36	205.8	14.1	2310	9 ADA00876	Ada00876 Mouse ESD
37	205.6	14.0	2020	10 ADA53293	Ada53293 Human cod
38	205.6	14.0	2046	3 AA251872	Aaz51872 Human Fac
39	205.6	14.0	6093	10 ADA19345	Ada19345 Human ins
40	205.6	14.0	6595	12 ADQ23685	Adq23685 Human sof
41	204	13.9	1562	8 ABX93043	Abx93043 Human LCC
42	204	13.9	2200	6 ABA00056	Abao0056 CADHP-3 c
43	204	13.9	2280	8 ABX93042	Abx93042 Human LCC
44	204	13.9	2328	9 ADA00874	Ada00874 Human ESD
45	204	13.9	2391	9 AAL62024	Aal62024 Human cel

ALIGNMENTS

RESULT 1

AAS00615

ID AAS00615 standard; cDNA; 1620 BP.

XX AAS00615;

XX 29-AUG-2001 (first entry)

XX Novel human protein (NHP) DNA sequence #3.

XX Novel human protein; NHP; CUB domain; extracellular domain; gene therapy;
KW obesity; high blood pressure; connective tissue disorder; infertility;
KW NHP-mediated pathway; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1620

FT /tag= a

FT /product= "Novel human protein #3"

XX WO200129219-A1.

XX 26-APR-2001.

XX 08-OCT-2000; 2000WO-US028798.

XX 19-OCT-1999; 99US-0160285P.

XX 18-FEB-2000; 2000US-0183583P.

XX (LEXI-) LEXICON GENETICS INC.

XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;

XX Sands AT;

XX WPI; 2001-290917/30.

XX P-PSDB; AAU00630.

XX Novel nucleic acid encoding human CUB-domain containing protein, useful
PT for drug screening, diagnosis and treatment of physiological disorders or
PT diseases.

PS Disclosure; Page 28-29; 33pp; English.

XX The sequence represents a polynucleotide which encodes a novel human
CC protein (NHP) containing a CUB domain (an extracellular domain). CUB
CC proteins have been associated with regulating development, modulating
CC cellular processes and preventing infectious disease. NHP nucleotide
CC sequences are useful for gene therapy of physiological disorders or
CC diseases. NHP oligonucleotides are useful as hybridisation probes for
CC screening libraries and assessing gene patterns. NHP nucleotide sequences
CC are useful for detecting mutant or inappropriately expressed NHPs (for
CC example, those proteins associated with obesity, high blood pressure,
CC connective tissue disorders and infertility) for the diagnosis of a
CC disease. The polynucleotides may also be used in screening for drugs
CC effective in the treatment of symptomatic or phenotypic manifestations of
CC perturbing the normal function of NHP in the body. Nucleotide constructs
CC encoding NHP products are used to genetically engineer host cells to
CC express such products in vivo. These host cells allow for the
CC identification of compounds that bind to NHP receptors or trigger NHP-
CC mediated pathways

XX SQ Sequence 1620 BP; 456 A; 353 C; 422 G; 389 T; 0 U; 0 Other;

Query March 100.0%; Score 1464; DB 4; Length 1620;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGACATCTAAGAAATTATCCCGGACCTACCCCAATCACACTGTTTGCAGAAAGACAATT 60
Db 157 ATGACATCTAAGAAATTATCCCGGACCTACCCCAATCACACTGTTTGCAGAAAGACAATT 216
Qy 61 ACAGTACCAAGGGGAAAGACTGATCTCAGGTTGGGAGATTGGATATCGAATCCAG 120
Db 217 ACAGTACCAAGGGGAAAGACTGATCTCAGGTTGGGAGATTGGATATCGAATCCAG 276
Qy 121 ACCTGTCTCTGACTATCTCTCTCCACAGCTCTTCAGATCAATATGTCATATCTGT 180
Db 277 ACCTGTCTCTGACTATCTCTCTCCACAGCTCTTCAGATCAATATGTCATATCTGT 336
Qy 181 GGAAGTATGACTGTCTCCAAAGAACTCTTGTGTGAACAACAAGTGAAGTAAACCGTCCGCTTT 240
Db 337 GGAAGTATGACTGTCTCCAAAGAACTCTTGTGTGAACAACAAGTGAAGTAAACCGTCCGCTTT 396
Qy 241 GAGAGTGGATCCCACTTTCTGGCGGGGTTTTTGTGCTGACCTATGCGAGCGGACCAT 300
Db 397 GAGAGTGGATCCCACTTTCTGGCGGGGTTTTTGTGCTGACCTATGCGAGCGGACCAT 456
Qy 301 CCAGATTTAATAACATGTTTGGAAACGAGTAGCCATTATTTGAAGACAGAAATACAGCAA 360
Db 457 CCAGATTTAATAACATGTTTGGAAACGAGTAGCCATTATTTGAAGACAGAAATACAGCAA 516
Qy 361 TTCTGCCAGCTGGTTGTAGAGAGTACGAGGAGACATTTCTGGGAAATATGGTAGATGGA 420
Db 517 TTCTGCCAGCTGGTTGTAGAGAGTACGAGGAGACATTTCTGGGAAATATGGTAGATGGA 576
Qy 421 TATAGAGATACCTCTTTATTTGTGAAAGCTGCCATCCATGCGAGGAATATTTGCTGATGAA 480
Db 577 TATAGAGATACCTCTTTATTTGTGAAAGCTGCCATCCATGCGAGGAATATTTGCTGATGAA 636
Qy 481 CTAGGTGCCAGATCAGTGTGCTTTCAGCGCAAGGGATCAGTCGATATGAAGGGATCTG 540
Db 637 CTAGGTGCCAGATCAGTGTGCTTTCAGCGCAAGGGATCAGTCGATATGAAGGGATCTG 696
Qy 541 GCCAATGGTGTCTTTTCAGGGATGGTTCCCTGTGACAGCAAGCGATTTCTGTTCCTCC 600
Db 697 GCCAATGGTGTCTTTTCAGGGATGGTTCCCTGTGACAGCAAGCGATTTCTGTTCCTCC 756
Qy 601 AATGGTTGCAGCAGATCCTTGAGTTTGAACCTGACCGGCAATCAGAGCTTCTTCTCTCA 660
Db 757 AATGGTTGCAGCAGATCCTTGAGTTTGAACCTGACCGGCAATCAGAGCTTCTTCTCTCA 816
Qy 661 TGGCAGTCCGTCATAGAGTGGAGACCAAGTTCACTTCTCTGCGCAAGCCGACCTT 720
Db 817 TGGCAGTCCGTCATAGAGTGGAGACCAAGTTCACTTCTCTGCGCAAGCCGACCTT 876

Qy 721 CAGGACCAAGGCCCATCATGGGCTTCGGCGCAGTAGCAACAACCAAAACACAGAG 780
Db 877 CAGGACCAAGGCCCATCATGGGCTTCGGCGCAGTAGCAACAACCAAAACACAGAG 936
Qy 781 TGGCTGGAGATCGATTTGGGGGAGAAAGAAATTAACAGGAATTAGGACCAAGATCT 840
Db 937 TGGCTGGAGATCGATTTGGGGGAGAAAGAAATTAACAGGAATTAGGACCAAGATCT 996
Qy 841 ACACAGTCCGAACCTTCAACTTTTATGTAAAGATTTTGTGATGAACCTTCAAAAACAATAAT 900
Db 997 ACACAGTCCGAACCTTCAACTTTTATGTAAAGATTTTGTGATGAACCTTCAAAAACAATAAT 1056
Qy 901 TCTAAGTGAAGACCTTATAAAGAAATTTGAATAATGAAGAAAGAGTGTTCAGGGTAAC 960
Db 1057 TCTAAGTGAAGACCTTATAAAGAAATTTGAATAATGAAGAAAGAGTGTTCAGGGTAAC 1116
Qy 961 TCTAAGTTCGGGACCCAGTGCAGAAACATTTTCATCCCTCCCATCGTGGCCAGATATG 1020
Db 1117 TCTAAGTTCGGGACCCAGTGCAGAAACATTTTCATCCCTCCCATCGTGGCCAGATATG 1176
Qy 1021 CGGGTTGTCCCCCAGACATGGCCACAGAGATAGCCTTGAAGGTGGAGCTCATTTGGTTGC 1080
Db 1177 CGGGTTGTCCCCCAGACATGGCCACAGAGATAGCCTTGAAGGTGGAGCTCATTTGGTTGC 1236
Qy 1081 CAGATTACACAAGGTAAATGATTCATTTGGTGTGGCGCAAGCAAGTCAAAAGCACAGTGT 1140
Db 1237 CAGATTACACAAGGTAAATGATTCATTTGGTGTGGCGCAAGCAAGTCAAAAGCACAGTGT 1296
Qy 1141 TCNACTTAAGAAAGAGATGAGCAATCAAGGCCCATCCCTCGGAAGAAACATCCACA 1200
Db 1297 TCNACTTAAGAAAGAGATGAGCAATCAAGGCCCATCCCTCGGAAGAAACATCCACA 1356
Qy 1201 GGAATAAAACATTAACAACGGTGGCTATTCATTTGGTGTCTCTTGTCTCTGTCTGTCT 1260
Db 1357 GGAATAAAACATTAACAACGGTGGCTATTCATTTGGTGTCTCTTGTCTCTGTCTGTCT 1416
Qy 1261 GGAATGGGATCTTTGCAGCCTTTAGAAAGAAAGAAAGAAAGAGTCCGTATGATCA 1320
Db 1417 GGAATGGGATCTTTGCAGCCTTTAGAAAGAAAGAAAGAAAGAGTCCGTATGATCA 1476
Qy 1321 GCGGAGCTCAGAAAACAGACTGTTGGAAGCAGATTAAATATCCCTTTGCGACACATCAG 1380
Db 1477 GCGGAGCTCAGAAAACAGACTGTTGGAAGCAGATTAAATATCCCTTTGCGACACATCAG 1536
Qy 1381 TCAGCTGAGTTTACCATCAGCTATGATTAATGAAGAGAGATGACACAAAAGTTAGATCTC 1440
Db 1537 TCAGCTGAGTTTACCATCAGCTATGATTAATGAAGAGAGATGACACAAAAGTTAGATCTC 1596
Qy 1441 ATCAAGTGAATGCGAGGTTAA 1464
Db 1597 ATCAAGTGAATGCGAGGTTAA 1620

RESULT 2

AAS00614
ID AAS00614 standard; cDNA; 1761 BP.

XX AAS00614;

AC AAS00614;

XX 29-AUG-2001 (first entry)

XX Novel human protein (NHP) DNA sequence #2.

XX Novel human protein; NHP; CUB domain; extracellular domain; gene therapy;

XX obesity; high blood pressure; connective tissue disorder; infertility;

XX NHP-mediated pathway; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..1761

XX /*tag= a

Db 1738 ATCAAGTGATATGCGAGTTAA 1761

RESULT 3
ID AAS00613 standard; DNA; 1768 BP.
AC AAS00613;
XX 29-AUG-2001 (first entry)
XX Novel human protein (NHP) DNA sequence #1.
DE
XX Novel human protein; NHP; CUB domain; extracellular domain; gene therapy;
KW obesity; high blood pressure; connective tissue disorder; infertility;
KW NHP-mediated pathway; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
FH 59..1522
FT CDS /tag= a
FT /product= "Novel human protein #1"
XX WO200129219-A1.
XX
XX 26-APR-2001.
XX 08-OCT-2000; 2000WO-US028798.
XX 19-OCT-1999; 99US-0160285P.
PR 18-FEB-2000; 2000US-0183583P.
XX (LEXI-) LEXICON GENETICS INC.
PA
XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
PI Sands AT;
XX WPI; 2001-290917/30.
DR P-PSDB; AAU00628.
XX
XX Novel nucleic acid encoding human CUB-domain containing protein, useful
PT for drug screening, diagnosis and treatment of physiological disorders or
PT diseases.
XX
XX Disclosure; Page 30-31; 33pp; English.
XX
XX The sequence represents a polynucleotide which encodes a novel human
CC protein (NHP) containing a CUB domain (an extracellular domain). CUB
CC proteins have been associated with regulating development, modulating
CC cellular processes and preventing infectious disease. NHP nucleotide
CC sequences are useful for gene therapy of physiological disorders or
CC diseases. NHP oligonucleotides are useful as hybridisation probes for
CC screening libraries and assessing gene patterns. NHP nucleotide sequences
CC are useful for detecting mutant or inappropriately expressed NHPs (for
CC example, those proteins associated with obesity, high blood pressure,
CC connective tissue disorders and infertility) for the diagnosis of a
CC disease. The polynucleotides may also be used in screening for drugs
CC effective in the treatment of symptomatic or phenotypic manifestations of
CC perturbing the normal function of NHP in the body. Nucleotide constructs
CC encoding NHP products are used to genetically engineer host cells to
CC express such products in vivo. These host cells allow for the
CC identification of compounds that bind to NHP receptors or trigger NHP-
CC mediated pathways
XX
XX Sequence 1768 BP; 539 A; 370 C; 421 G; 438 T; 0 U; 0 Other;
Query Match 100.0%; Score 1464; DB 4; Length 1768;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 ATGACATCTAAGAAATTATCCCGGACCTACCCCAATCACACTGTTTCGAAAAGACAATT 60

Db 59 ATGACATCTAAGAAATTATCCCGGACCTACCCCAATCACACTGTTTCGAAAAGACAATT 118
QY 61 ACAGTACCAAAGGGGAAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCCCAG 120
Db 119 ACAGTACCAAAGGGGAAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCCCAG 178
QY 121 ACCTGTGCTTCTGACTATCTTCTTCCACAGCTCTTCTGATCAATATGCTCATCTGT 180
Db 179 ACCTGTGCTTCTGACTATCTTCTTCCACAGCTCTTCTGATCAATATGCTCATCTGT 238
QY 181 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTAACACAAAGTGAAGTAAACCTGCGCTTT 240
Db 239 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTAACACAAAGTGAAGTAAACCTGCGCTTT 298
QY 241 GAGAGTGATCCCAACATTTCTGCGCGGGGTTTTTGTGCTGACCTATGCGAGCAGCGACCAT 300
Db 299 GAGAGTGGATCCCAACATTTCTGCGCGGGGTTTTTGTGCTGACCTATGCGAGCAGCGACCAT 358
QY 301 CCAGATTAAATCAATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAAA 360
Db 359 CCAGATTAAATCAATGTTTGGAAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAAA 418
QY 361 TTCTGCCCAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGGAATATGTTAGATGGA 420
Db 419 TTCTGCCCAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGGAATATGTTAGATGGA 478
QY 421 TATAGAGATACCTCTTTTATTTGTCAAAGCTGCCATCCATGCAAGGAATAATTTGCTGATGA 480
Db 479 TATAGAGATACCTCTTTTATTTGTCAAAGCTGCCATCCATGCAAGGAATAATTTGCTGATGA 538
QY 481 CTAGTGGCCAGATCAGTGTCTTACGCCAAAGGGATCAGTCGATATGAAGGGATTTCTG 540
Db 539 CTAGTGGCCAGATCAGTGTCTTACGCCAAAGGGATCAGTCGATATGAAGGGATTTCTG 598
QY 541 GCCAATGGTGTCTTTCGAGGAGTGGTCCCTGTCAGACAAGGATTTCTGTTTACTCTCC 600
Db 599 GCCAATGGTGTCTTTCGAGGAGTGGTCCCTGTCAGACAAGGATTTCTGTTTACTCTCC 658
QY 601 AATGGTTGCAGCAGATCCTTTGAACTTTGAACTGACGGGCAAAATCAGAGCTTCTTCTCTCA 660
Db 659 AATGGTTGCAGCAGATCCTTTGAACTTTGAACTGACGGGCAAAATCAGAGCTTCTTCTCTCA 718
QY 661 TGCCAGTCTGGTCAATGAGAGTGGAGACCAAGTTCACTGGTCTCTCGGCCAAGCCGACTT 720
Db 719 TGCCAGTCTGGTCAATGAGAGTGGAGACCAAGTTCACTGGTCTCTCGGCCAAGCCGACTT 778
QY 721 CAGGACCAAGGCCCATCATGGGCTTCGGGCGCAGTAGCAACAACCAACCAACCCAGAG 780
Db 779 CAGGACCAAGGCCCATCATGGGCTTCGGGCGCAGTAGCAACAACCAACCAACCCAGAG 838
QY 781 TGCTCTGGAGATCGATTTGGGGGAGAAAAGAAATAACAGGAATTAGGACCAAGATCT 840
Db 839 TGCTCTGGAGATCGATTTGGGGGAGAAAAGAAATAACAGGAATTAGGACCAAGATCT 898
QY 841 ACACAGTCGAACTTCAACTTTATGTTAGAGTTTTGTGATGAATTTCAAAAAAATAAT 900
Db 899 ACACAGTCGAACTTCAACTTTATGTTAGAGTTTTGTGATGAATTTCAAAAAAATAAT 958
QY 901 TCTAAGTGGAGACCTATAAAGGAAATTTGTAATAATGAAGAAAAGGTGTTTCAGGGTAAAC 960
Db 959 TCTAAGTGGAGACCTATAAAGGAAATTTGTAATAATGAAGAAAAGGTGTTTCAGGGTAAAC 1018
QY 961 TCTAAGTGGAGACCTATAAAGGAAATTTGTAATAATGAAGAAAAGGTGTTTCAGGGTAAAC 1020
Db 1019 TCTAAGTGGAGACCTATAAAGGAAATTTGTAATAATGAAGAAAAGGTGTTTCAGGGTAAAC 1078
QY 1021 CGGGTTGTCCCCAGACATGGCCACGAGAGATAGCTTTGAGGTGAGCTCATTTGGTTGC 1080
Db 1079 CGGGTTGTCCCCAGACATGGCCACGAGAGATAGCTTTGAGGTGAGCTCATTTGGTTGC 1138
QY 1081 CAGATTACACAAGGTAAATGATTTCATTTGGTGGCGGAAGCAAGTCAAAAGCACCAGTGT 1140

Db 1139 CAGATTACACAAGTAATGATTCATTGGTGTGGCGCAAGACAAAGTCAAAGCCAGCGTT 1198
Qy 1141 TCAACTAAGAAGAGATGAGACATCACAGGCCCATCCCTCGGAAGAAACATCCACA 1200
Db 1199 TCAACTAAGAAGAGATGAGACATCACAGGCCCATCCCTCGGAAGAAACATCCACA 1258
Qy 1201 GGAATAAACATTCAACCGTGGCTATTCCATTGGTGTCTCTTGTGTCTGGTGTGGCT 1260
Db 1259 GGAATAAACATTCAACCGTGGCTATTCCATTGGTGTCTCTTGTGTCTGGTGTGGCT 1318
Qy 1261 GGAATGGGATCTTTGAGCGCTTTAGAAAGAGAGAAAGAAAGTCCGTATGATCA 1320
Db 1319 GGAATGGGATCTTTGAGCGCTTTAGAAAGAGAGAAAGAAAGTCCGTATGATCA 1378
Qy 1321 GCGGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAAATATCCCTTTGCCAGACATCAG 1380
Db 1379 GCGGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAAATATCCCTTTGCCAGACATCAG 1438
Qy 1381 TCAGCTGAGTTTACCATCAGCTATGATPAATGAGAAGGAGATGACACAAAAGTTAGATCTC 1440
Db 1439 TCAGCTGAGTTTACCATCAGCTATGATPAATGAGAAGGAGATGACACAAAAGTTAGATCTC 1498
Qy 1441 ATCACAAGTCATATGCGAGGTTAA 1464
Db 1499 ATCACAAGTCATATGCGAGGTTAA 1522

RESULT 4

ADN39765

ID ADN39765 standard; cDNA; 1761 BP.

AC ADN39765;

XX 17-JUN-2004 (first entry)

DT Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C137.

DE Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnery; gene therapy; vaccine; gene; ss.

XX Homo sapiens.

XX WO2003042661-A2.

PN 22-MAY-2003.

XX 13-NOV-2001; 2001US-0350666P.

XX 21-NOV-2001; 2001US-0332464P.

XX 29-NOV-2001; 2001US-0334393P.

XX 03-DEC-2001; 2001US-0335394P.

XX 14-DEC-2001; 2001US-0340376P.

XX 08-JAN-2002; 2002US-0347211P.

XX 10-FEB-2002; 2002US-0347349P.

XX 10-FEB-2002; 2002US-0355250P.

XX 13-FEB-2002; 2002US-0356714P.

XX 20-FEB-2002; 2002US-0359077P.

XX 29-MAR-2002; 2002US-0368809P.

XX 04-APR-2002; 2002US-0370110P.

XX 12-APR-2002; 2002US-0372246P.

XX 05-JUN-2002; 2002US-0386614P.

XX 16-JUL-2002; 2002US-0396839P.

XX 22-JUL-2002; 2002US-0397757P.

XX 22-JUL-2002; 2002US-0397845P.

XX 09-SEP-2002; 2002US-0409450P.

XX (E05B-) EOS BIOTECHNOLOGY INC.

XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX WPI; 2003-468649/44.
DR P-PSDB; ADN39982.
XX Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.

XX Claim 8; SEQ ID NO C137; 1385pp; English.

XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a nucleic acid sequence of the invention.

XX SQ Sequence 1761 BP; 472 A; 402 C; 482 G; 405 T; 0 U; 0 Other;

Query Match 99.9%; Score 1462.4; DB 11; Length 1761;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGACATCTAAGAAATTTATCCGGGACCTACCCCAATCACACTCTTTGCGAAAAGACAATT 60
Db 298 ATGACATCTAAGAAATTTATCCGGGACCTACCCCAATCACACTCTTTGCGAAAAGACAATT 357
Qy 61 ACAGTACCAAGGGGAAAAGACTGATTTCTGAGGTGGGAGATTGGATATCGAATCCCAG 120
Db 358 ACAGTACCAAGGGGAAAAGACTGATTTCTGAGGTGGGAGATTGGATATCGAATCCCAG 417
Qy 121 ACCTGTCTTCTGACTATCTTCTTCCAGCAGCTCTTCAGATCAATATGGTCCATCTGT 180
Db 418 ACCTGTCTTCTGACTATCTTCTTCCAGCAGCTCTTCAGATCAATATGGTCCATCTGT 477
Qy 181 GGAAGTATGACTGTTCCCAAGAACTCTTTGTAACAACAAGTGAAGTAAACCGTCGCTTT 240
Db 478 GGAAGTATGACTGTTCCCAAGAACTCTTTGTAACAACAAGTGAAGTAAACCGTCGCTTT 537
Qy 241 GAGAGTGGATCCCAATTTCTGCGGGGGTTTTTCTGACCTATCGGAGCAGCAGCAT 300
Db 538 GAGAGTGGATCCCAATTTCTGCGGGGGTTTTTCTGACCTATCGGAGCAGCAGCAT 597
Qy 301 CCAGATTTAATACATGTTTGGACAGCTAGCCATTTATTTGAGACAGNATACAGCAAA 360
Db 598 CCAGATTTAATACATGTTTGGAAACGAGCTAGCCATTTATTTGAGACAGNATACAGCAAA 657
Qy 361 TTCTGCCAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 420
Db 658 TTCTGCCAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 717
Qy 421 TATAGAGATACCTCTTTTATTTGTGCAAGCTGCCATCCATCGAGGAATAATTGCTGATGA 480
Db 718 TATAGAGATACCTCTTTTATTTGTGCAAGCTGCCATCCATCGAGGAATAATTGCTGATGA 777
Qy 481 CTAGTGGCCAGATCAGTGTGCTTACGCGAAAGGATCAGTGCATATGAGGAGATCTG 540
Db 778 CTAGTGGCCAGATCAGTGTGCTTACGCGAAAGGATCAGTGCATATGAGGAGATCTG 837

Matches 1463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	1	ATGACATCTAAGAAATTTATCCGGGACCTACCCCAATCACACTCTTTGCGGAAGACAAT	60
DB	282	ATGACATCTAAGAAATTTATCCGGGACCTACCCCAATCACACTCTTTGCGGAAGACAAT	341
QY	61	ACAGTACCAAAAGGGGAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCAG	120
DB	342	ACAGTACCAAAAGGGGAAAGACTGATTTCTGAGGTTGGGAGATTTGGATATCGAATCCAG	401
QY	121	ACCTGTGCTTCTGACTATCTTCTTCCACGAGCTCTTCAGATCAATATGGTCCATCTGT	180
DB	402	ACCTGTGCTTCTGACTATCTTCTTCCACGAGCTCTTCAGATCAATATGGTCCATCTGT	461
QY	181	GGAGTATGACTGTTCCCAAGAACTCTTGTGCAACACAGTGAAGTAAACCGTCCGCTTT	240
DB	462	GGAGTATGACTGTTCCCAAGAACTCTTGTGCAACACAGTGAAGTAAACCGTCCGCTTT	521
QY	241	GAGAGTGGATCCACATTTCTGGCCGGGTTTTTGTCTGACCTATCGAGCAGCGACCAT	300
DB	522	GAGAGTGGATCCACATTTCTGGCCGGGTTTTTGTCTGACCTATCGAGCAGCGACCAT	581
QY	301	CCAGATTTAATACATGTTTGGACGAGCTAGCCATTTTGAAGACAGATACAGCAAA	360
DB	582	CCAGATTTAATACATGTTTGGACGAGCTAGCCATTTTGAAGACAGATACAGCAAA	641
QY	361	TTCTGCCAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGTTAGATGA	420
DB	642	TTCTGCCAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGTTAGATGA	701
QY	421	TATAGAGATACCTCTTTATTTGTGCAAGCTGCCATCCATCGAGGAATAATTTGCTGATGA	480
DB	702	TATAGAGATACCTCTTTATTTGTGCAAGCTGCCATCCATCGAGGAATAATTTGCTGATGA	761
QY	481	CTAGTGGCCAGATCAGTGTCTTACGCCAAGGGATCAGTCGATATGAAGGATCTTG	540
DB	762	CTAGTGGCCAGATCAGTGTCTTACGCCAAGGGATCAGTCGATATGAAGGATCTTG	821
QY	541	GCAATGTTGTTCTTTTCGAGGAGTGTCTCCCTGTGACAGACGATTTCTGTTTACCTCC	600
DB	822	GCAATGTTGTTCTTTTCGAGGAGTGTCTCCCTGTGACAGACGATTTCTGTTTACCTCC	881
QY	601	AATGTTGACAGATCTTCTGAGTTTGAACCTGACGGCAATCAGAGCTTCTTCTCTCA	660
DB	882	AATGTTGACAGATCTTCTGAGTTTGAACCTGACGGCAATCAGAGCTTCTTCTCTCA	941
QY	661	TGCGAGTGGTCAATGAGAGTGAGACCAAGTTCTGTCCTGGCCAAAGCCGACTT	720
DB	942	TGCGAGTGGTCAATGAGAGTGAGACCAAGTTCTGTCCTGGCCAAAGCCGACTT	1001
QY	721	CAGGACCAAGGCCCATCATGGGCTTCGGGCGACGTAGCAACACCAACACGAGAG	780
DB	1002	CAGGACCAAGGCCCATCATGGGCTTCGGGCGACGTAGCAACACCAACACGAGAG	1061
QY	781	TGCGTGGAGATCGATTTGGGGGAGAAAAAGAAATAACAGGAATTAGGACCAAGATCT	840
DB	1062	TGCGTGGAGATCGATTTGGGGGAGAAAAAGAAATAACAGGAATTAGGACCAAGATCT	1121
QY	841	ACAGTGGAACTTCAACTTTTATGTAAGAGTTTGTGATGAATTTCAAAAACAATAAT	900
DB	1122	ACAGTGGAACTTCAACTTTTATGTAAGAGTTTGTGATGAATTTCAAAAACAATAAT	1181
QY	901	TCTAAGTGAAGACCTATTAAGGAATTGTGAATAATGAAGAAAGTGTTCAGGGTAA	960
DB	1182	TCTAAGTGAAGACCTATTAAGGAATTGTGAATAATGAAGAAAGTGTTCAGGGTAA	1241
QY	961	TCTAACTTTTGGGACCCAGTGCACAAATTTTATCTCCCTCCCATCGTGCCAGATATG	1020
DB	1242	TCTAACTTTTGGGACCCAGTGCACAAATTTTATCTCCCTCCCATCGTGCCAGATATG	1301
QY	1021	CGGGTTGTTCCCGACATGGCACCGAGGATAGCCTTGAAGGTGAGCTCATTTGGTTGC	1080
DB	1302	CGGGTTGTTCCCGACATGGCACCGAGGATAGCCTTGAAGGTGAGCTCATTTGGTTGC	1361

QY	1081	CAGATTACACAAGGTAATGATTCATTTGGTGTGCGCAAGCAAGTCAAAAGCACCAGTGT	1140
DB	1362	CAGATTACACAAGGTAATGATTCATTTGGTGTGCGCAAGCAAGTCAAAAGCACCAGTGT	1421
QY	1141	TCAACTAAGAAAGAAAGATGAGACAATCAACAAGGCCCATCCCTTCGGAAGAAACATCCACA	1200
DB	1422	TCAACTAAGAAAGAAAGATGAGACAATCAACAAGGCCCATCCCTTCGGAAGAAACATCCACA	1481
QY	1201	GGAAATAAATTTACAACGGTGGCTATTCATTTGGTGTCTCTTGTCTCTGTTGCTTGTCT	1260
DB	1482	GGAAATAAATTTACAACGGTGGCTATTCATTTGGTGTCTCTTGTCTCTGTTGCTTGTCT	1541
QY	1261	GGAAATGGGATCTTTTGCAGCCCTTTGAAAGAAAGAAAGAAAGAAAGTCCGTATGGATCA	1320
DB	1542	GGAAATGGGATCTTTTGCAGCCCTTTGAAAGAAAGAAAGAAAGAAAGTCCGTATGGATCA	1601
QY	1321	GGGAGGCTCAGAAAAACAGACTGTTTGGAAAGCAGATTTAAATATCCCTTTGCCAGACATCAG	1380
DB	1602	GGGAGGCTCAGAAAAACAGACTGTTTGGAAAGCAGATTTAAATATCCCTTTGCCAGACATCAG	1661
QY	1381	TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAAGTTAGATCTC	1440
DB	1662	TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAAGTTAGATCTC	1721
QY	1441	ATCACAAAGTGATATGCGAGTTTAA 1464	
DB	1722	ATCACAAAGTGATATGCGAGTTTAA 1745	
RESULT 6			
ADR46610			
ID	ADR46610 standard; DNA; 2010 BP.		
XX	ADR46610;		
AC			
DT	18-NOV-2004 (first entry)		
XX			
DE	Cancer-associated protein coding sequence, SEQ ID 23.		
XX			
KW	Cytostatic; Gene Therapy; cancer; human; gene; ds.		
OS	Homo sapiens.		
XX			
PH	Location/Qualifiers		
FT	126..1745		
FT	/*tag= a		
FT	/product= "Cancer-associated protein, SEQ ID 81"		
XX			
PN	WO2004073657-A2.		
XX			
PD	02-SEP-2004.		
XX			
PF	19-FEB-2004; 2004WO-US005455.		
XX			
PR	19-FEB-2003; 2003US-0448784P.		
XX			
PA	(PROT-) PROTEIN DESIGN LABS INC.		
XX			
PI	Aziz N, Gish KC, Wilson KE, Zlotnik A;		
XX			
DR	WPI; 2004-652787/63.		
XX			
DR	P-PSDB; ADR46668.		
XX			
PT	Detecting a pathological cell in a patient for diagnosing or treating		
PT	cancer by detecting in a biological sample from the patient genes whose		
-PT	expression are up-regulated or down-regulated in specific cancers.		
XX			
PS	Claim 1; SEQ ID NO 23; 375pp; English.		
XX			
CC	The present invention relates to a method for detecting cancer in a		
CC	patient. The method comprises detecting in a biological sample from the		
CC	patient a nucleotide or protein sequence comprising a sequence that is at		

CC least 80% identical to a nucleotide sequence (ADR46588-ADR46645) or
CC protein sequence (ADR46616-ADR46703). The method is useful for detecting
CC cancer for preparing a composition for diagnosing or treating cancer.
XX
SQ Sequence 2010 BP; 577 A; 457 C; 512 G; 464 T; 0 U; 0 Other;

Query Match 99.9%; Score 1462.4; DB 13; Length 2010;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGACATCTAAGAAATATCCCGGAGCTACCCCAATCACAATCTTTGCGAAAGACAAT 60
DB 282 ATGACATCTAAGAAATATCCCGGAGCTACCCCAATCACAATCTTTGCGAAAGACAAT 341

QY 61 ACAGTACCAAGGGGAAAGACTGATCTGAGGTGGGAGATTGGATATCGAATCCCGAG 120
DB 342 ACAGTACCAAGGGGAAAGACTGATCTGAGGTGGGAGATTGGATATCGAATCCCGAG 401

QY 121 ACCTGTGCTTCTGACTATCTTCTTCCACAGCTCTTCCAGATCAATATGTCCTACTGT 180
DB 402 ACCTGTGCTTCTGACTATCTTCTTCCACAGCTCTTCCAGATCAATATGTCCTACTGT 461

QY 181 GGAAGTATGACTGTTCCCAAGAACTCTTGTGGAACAAGTGAAGTAAACCGTCCGCTTT 240
DB 462 GGAAGTATGACTGTTCCCAAGAACTCTTGTGGAACAAGTGAAGTAAACCGTCCGCTTT 521

QY 241 GAGAGTGGATCCCAATTTCTGCGCGGGTCTTGTGCTGACCTATGCGAGCAGACCAT 300
DB 522 GAGAGTGGATCCCAATTTCTGCGCGGGTCTTGTGCTGACCTATGCGAGCAGACCAT 581

QY 301 CCAGATTAAATAACATGTTTGGACAGCTAGCCATTTATGGAAGACAGAAATACAGAAA 360
DB 582 CCAGATTAAATAACATGTTTGGACAGCTAGCCATTTATGGAAGACAGAAATACAGAAA 641

QY 361 TTCTGCCAGCTGTTAGAGAGCTAGCAGAGACATTTCTGGAATATGTTAGATGGA 420
DB 642 TTCTGCCAGCTGTTAGAGAGCTAGCAGAGACATTTCTGGAATATGTTAGATGGA 701

QY 421 TATAGATACCTCTTATTTATGTCGAAAGCTGCCATCATGAGGAATAATTTGCTGATGAA 480
DB 702 TATAGATACCTCTTATTTATGTCGAAAGCTGCCATCATGAGGAATAATTTGCTGATGAA 761

QY 481 CTAGTGGCCAGATCAGTGTCTTTCAGCGCAAGGGATCAGTCGATATGAAGGATCTG 540
DB 762 CTAGTGGCCAGATCAGTGTCTTTCAGCGCAAGGGATCAGTCGATATGAAGGATCTG 821

QY 541 GCCAATGGTCTTCTTCAGGGATGGTTCCTGTGACAGACGATTTCTGTTTACCTCC 600
DB 822 GCCAATGGTCTTCTTCAGGGATGGTTCCTGTGACAGACGATTTCTGTTTACCTCC 881

QY 601 AATGGTTGACAGATCCTTCTGAGTTTGAACCTGACGGCAAAATCAGAGCTTCTTCTCTCA 660
DB 882 AATGGTTGACAGATCCTTCTGAGTTTGAACCTGACGGCAAAATCAGAGCTTCTTCTCTCA 941

QY 661 TGGCAGTGGTCAATAGAGATGGAGACCAAGTTCACTGGTCTCTGCGCAAGCCGACTT 720
DB 942 TGGCAGTGGTCAATAGAGATGGAGACCAAGTTCACTGGTCTCTGCGCAAGCCGACTT 1001

QY 721 CAGACACAGGCCCATCATGGGCTTCGGGCGACAGTAGCACAACCAACCAACAGAGAG 780
DB 1002 CAGACACAGGCCCATCATGGGCTTCGGGCGACAGTAGCACAACCAACCAACAGAGAG 1061

QY 781 TGGCTGGAGATCGATTTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACACAGGATCT 840
DB 1062 TGGCTGGAGATCGATTTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACACAGGATCT 1121

QY 841 ACACAGTGGAACTTCAACTTTATGTTAAGAGTTTGTGATGAATCCAAAACAAATAT 900
DB 1122 ACACAGTGGAACTTCAACTTTATGTTAAGAGTTTGTGATGAATCCAAAACAAATAT 1181

QY 901 TCTAAGTGGAGACCTATAAGGAATTTGTAATATGAAGAAAGGTGTTTCAGGGTAAC 960
DB 1182 TCTAAGTGGAGACCTATAAGGAATTTGTAATATGAAGAAAGGTGTTTCAGGGTAAC 1241

QY 961 TCTAACTTTTCGGGACCCAGTGCAGAAACAATTTTCATCTCCCTCCATCGTGGCCAGATATGTG 1020
DB 1242 TCTAACTTTTCGGGACCCAGTGCAGAAACAATTTTCATCTCCCTCCATCGTGGCCAGATATGTG 1301

QY 1021 CGGGTTGTCCCCAGACATGGCCAGAGGATAGCTTTGAAGGTGGAGCTCATTTGGTTGC 1080
DB 1302 CGGGTTGTCCCCAGACATGGCCAGAGGATAGCTTTGAAGGTGGAGCTCATTTGGTTGC 1361

QY 1081 CAGATTACACAAGGTAATGATTCAATTTGGTGTGGCGCAAGCAAGTCAAAAGCACCAGTGT 1140
DB 1362 CAGATTACACAAGGTAATGATTCAATTTGGTGTGGCGCAAGTCAAAAGCACCAGTGT 1421

QY 1141 TCAACTAAGAAAAGAGATGAGACAATCACAAGGCCCATCCCTCGGAAGAAACATCCACA 1200
DB 1422 TCAACTAAGAAAAGAGATGAGACAATCACAAGGCCCATCCCTCGGAAGAAACATCCACA 1481

QY 1201 GGAATTAACAATTTACACGGTGGCTATTTCCATTTGGTGTCTCTTGTCTCTGGTGTGCT 1260
DB 1482 GGAATTAACAATTTACACGGTGGCTATTTCCATTTGGTGTCTCTTGTCTCTGGTGTGCT 1541

QY 1261 GGAATGGGATCTTTTCAGCGCTTTTGAAGAAAGAAAGAAAGAAAGTCCGTATGATCA 1320
DB 1542 GGAATGGGATCTTTTCAGCGCTTTTGAAGAAAGAAAGAAAGAAAGTCCGTATGATCA 1601

QY 1321 GCGAGGCTCAGAAAACAGACTGTTGGAAAGCAGATTAAATATATCCCTTGGCCAGACATCAG 1380
DB 1602 GCGAGGCTCAGAAAACAGACTGTTGGAAAGCAGATTAAATATATCCCTTGGCCAGACATCAG 1661

QY 1381 TCAGCTGAGTTTACCATCAGCTATGATATGAAAGAGAGATGACACAAAAGTTAGATCTC 1440
DB 1662 TCAGCTGAGTTTACCATCAGCTATGATATGAAAGAGAGATGACACAAAAGTTAGATCTC 1721

QY 1441 ATCACAAGTGATATGCGAGTTAA 1464
DB 1722 ATCACAAGTGATATGCGAGTTAA 1745

RESULT 7
ADR46611
ID ADR46611 standard; DNA; 2010 BP.
XX ADR46611;
XX
XX 18-NOV-2004 (first entry)
XX
XX Cancer-associated protein coding sequence, SEQ ID 24.
XX Cytostatic; Gene Therapy; cancer; human; gene; ds.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 126..1745
XX /*tag= a
XX /product= "Cancer-associated protein, SEQ ID 82"
XX
XX WO2004073657-A2.
XX
XX 02-SEP-2004.
XX
XX 19-FEB-2004; 2004MO-US005455.
XX
XX 19-FEB-2003; 2003US-0448784P.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Aziz N, Gish KC, Wilson KB, Zlotnik A;
XX WPI; 2004-652787/63.
XX P-PSDB; ADR46669.
XX
XX Detecting a pathological cell in a patient for diagnosing or treating

cancer by detecting in a biological sample from the patient genes whose expression are up-regulated or down-regulated in specific cancers.

Claim 1; SEQ ID NO 24; 375pp; English.

The present invention relates to a method for detecting cancer in a patient. The method comprises detecting in a biological sample from the patient a nucleotide or protein sequence comprising a sequence that is at least 80% identical to a nucleotide sequence (ADR46588-ADR46645) or protein sequence (ADR46646-ADR46703). The method is useful for detecting cancer for preparing a composition for diagnosing or treating cancer.

Sequence 2010 BP; 577 A; 457 C; 512 G; 464 T; 0 U; 0 Other;

Query Match	99.9%;	Score	1462.4;	DB	13;	Length	2010;
Best Local Similarity	99.9%;	Pred. No.	0;				
Matches	1463;	Conservative	0;	Mismatches	1;	Indels	0;
Gaps	0;						
QY	1	ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACA	CTGTTTTCGGAAGACAAAT	60			
DB	282	ATGACATCTAAGAAATATCCCGGACCTACCCCAATCACA	CTGTTTTCGGAAGACAAAT	341			
QY	61	ACAGTACCAAGGGGAAGAGACTGATCTGAGGTTGGAGAT	TGGATATCGAATCCAG	120			
DB	342	ACAGTACCAAGGGGAAGAGACTGATCTGAGGTTGGAGAT	TGGATATCGAATCCAG	401			
QY	121	ACCTGTGCTTCTGACTATCTCTTCCACCAGCTCTTCAGAT	CAATATGTCCTACTGT	180			
DB	402	ACCTGTGCTTCTGACTATCTCTTCCACCAGCTCTTCAGAT	CAATATGTCCTACTGT	461			
QY	181	GGAGTATGACTGTTCCCAAGAACTCTTGTGGAACAAGTGA	AGTAACCGTCCGCTTT	240			
DB	462	GGAGTATGACTGTTCCCAAGAACTCTTGTGGAACAAGTGA	AGTAACCGTCCGCTTT	521			
QY	241	GAGAGTGGATCCACATTTCTGCGCGGGTCTTTCGTGAC	TACCTATCGGAGCGAGCAAT	300			
DB	522	GAGAGTGGATCCACATTTCTGCGCGGGTCTTTCGTGAC	TACCTATCGGAGCGAGCAAT	581			
QY	301	CCAGATTTAATACATGTTTGGAAACGAGCTAGCCATTTAT	TGGAAGACAGATACACAAA	360			
DB	582	CCAGATTTAATACATGTTTGGAAACGAGCTAGCCATTTAT	TGGAAGACAGATACACAAA	641			
QY	361	TTCTGCCAGCTGTTGTAGACGCTAGCAGGAGACATTTCT	GGGAATATGGTAGGA	420			
DB	642	TTCTGCCAGCTGTTGTAGACGCTAGCAGGAGACATTTCT	GGGAATATGGTAGGA	701			
QY	421	TATAGATACCTCTTTATTTGCAAGCTGCCATCATGCAAG	ATATATGCTGATGA	480			
DB	702	TATAGATACCTCTTTATTTGCAAGCTGCCATCATGCAAG	ATATATGCTGATGA	761			
QY	481	CTAGGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGAT	CAGTCGATATGAAGGATCTG	540			
DB	762	CTAGGTGGCCAGATCAGTGTGCTTTCAGCGCAAGGGAT	CAGTCGATATGAAGGATCTG	821			
QY	541	GCAATGTTGTTCTTTTCGAGGATGTTTCCCTGTACACA	AGCGATTTCTGTTTACCTCC	600			
DB	822	GCAATGTTGTTCTTTTCGAGGATGTTTCCCTGTACACA	AGCGATTTCTGTTTACCTCC	881			
QY	601	AATGTTGAGCAGATCTTGTAGTTTGAACCTGACGGGCA	ATCAGAGCTTCTTCTCA	660			
DB	882	AATGTTGAGCAGATCTTGTAGTTTGAACCTGACGGGCA	ATCAGAGCTTCTTCTCA	941			
QY	661	TGCGCTCGGTCAATGAGAGTGGAGACCAAGTTTCACT	GGTCTCTGCGCAAGCCGACTT	720			
DB	942	TGCGCTCGGTCAATGAGAGTGGAGACCAAGTTTCACT	GGTCTCTGCGCAAGCCGACTT	1001			
QY	721	CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAG	CAACCAACCAACCCAGAG	780			
DB	1002	CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAG	CAACCAACCAACCCAGAG	1061			
QY	781	TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAATAA	AGGAATTAAGGACCAAGATCT	840			
DB	1062	TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAATAA	AGGAATTAAGGACCAAGATCT	1121			

QY	841	ACACAGTGGAACTTCAACTTTTATGTTTAAGAGTTTGTG	ATGAACCTTCAAAAAACAATAAT	900
DB	1122	ACACAGTGGAACTTCAACTTTTATGTTTAAGAGTTTGTG	ATGAACCTTCAAAAAACAATAAT	1181
QY	901	TCTAAGTGGAAAGACCTTATAAGGAATTTGTAATAAT	GAAGAAAGGTGTTTCAGGGTAAC	960
DB	1182	TCTAAGTGGAAAGACCTTATAAGGAATTTGTAATAAT	GAAGAAAGGTGTTTCAGGGTAAC	1241
QY	961	TCTAAGTGGAAAGACCTTATAAGGAATTTGTAATAAT	GAAGAAAGGTGTTTCAGGGTAAC	1020
DB	1242	TCTAAGTGGAAAGACCTTATAAGGAATTTGTAATAAT	GAAGAAAGGTGTTTCAGGGTAAC	1301
QY	1021	CGGGTGTCTCCCGCAGACATGGCACAGAGATAGCTT	CAAGGTGAGCTCATTTGGTTGC	1080
DB	1302	CGGGTGTCTCCCGCAGACATGGCACAGAGATAGCTT	CAAGGTGAGCTCATTTGGTTGC	1361
QY	1081	CAGATTACACAAGGTAAATGATTCATTTGGTGTGGCG	CAAGCAAGTCAAGCACCAGTGT	1140
DB	1362	CAGATTACACAAGGTAAATGATTCATTTGGTGTGGCG	CAAGCAAGTCAAGCACCAGTGT	1421
QY	1141	TCAACTTAAGAAAGAGATGAGCAATTCACAGGCCCAT	CCCCCTCGGAAGAAACATCCACA	1200
DB	1422	TCAACTTAAGAAAGAGATGAGCAATTCACAGGCCCAT	CCCCCTCGGAAGAAACATCCACA	1481
QY	1201	CGAATAAAACATTTACAAACGGTGGCTATTCCATTGG	TGCTCTCTTGTCTTGGTGTGCT	1260
DB	1482	CGAATAAAACATTTACAAACGGTGGCTATTCCATTGG	TGCTCTCTTGTCTTGGTGTGCT	1541
QY	1261	GGAAATGGGATCTTTTGACGCTTTTGAAGAAAGAAAG	AAAGTCCGTATGGATCA	1320
DB	1542	GGAAATGGGATCTTTTGACGCTTTTGAAGAAAGAAAG	AAAGTCCGTATGGATCA	1601
QY	1321	GGGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTA	ATAATATCCCTTTCGACACATCAG	1380
DB	1602	GGGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTA	ATAATATCCCTTTCGACACATCAG	1661
QY	1381	TCAGCTGAGCTTTTACCATCAGCTATGATAATGAGN	AGGAGATGACACAAAAGTTAGATCTC	1440
DB	1662	TCAGCTGAGCTTTTACCATCAGCTATGATAATGAGN	AGGAGATGACACAAAAGTTAGATCTC	1721
QY	1441	ATCACAAGTGTATATGCGAGTTAA	1464	
DB	1722	ATCACAAGTGTATATGCGAGTTAA	1745	

RESULT 8

ACD66718

ID ACD66718 standard; cdna; 2145 BP.

XX ACD66718;

XX AC

XX DT 17-SEP-2003 (first entry)

XX Secreted polypeptide-related cdna #10.

DE Human; gene; ss; TANGO; INTERCEPT; secreted polypeptide; immune disorder;
XX hormonal disorder; proliferative disorder; cancer; thyroid disorder;
XX diabetes; multiple sclerosis; lupus; neurological disorder; anaemia;
XX Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
XX myocardial infarction; congestive heart disease; blood platelet disorder;
XX thrombocytopenia; blood vessel; atherosclerosis; vasculitis.

OS Homo sapiens.

XX US2003022279-A1.

XX 30-JAN-2003.

XX 12-JAN-2001; 2001US-00759130.

XX 14-JUN-1999; 99US-00333159.

XX 29-JUN-1999; 99US-00342364.

PR 10-SEP-1999; 99US-00393996.
PR 19-OCT-1999; 99US-00420707.
PR 07-JAN-2000; 2000US-00479249.
PR 27-APR-2000; 2000US-00559497.
PR 24-MAY-2000; 2000US-00578063.
PR 16-JUN-2000; 2000US-00596194.
PR 23-JUN-2000; 2000US-00602871.
PR 30-JUN-2000; 2000US-00608452.
XX (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
XX (GOOD/) GOODEARL A D J.
XX Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR,
PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;
XX P-PSDB; ABO32527.
DR WPI: 2003-456290/43.
XX New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,
PT TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or
PT treating disorders such as cancer, diabetes or atherosclerosis, and in
PT forensic biology.
XX Claim 2; Fig 10A-10B; 482pp; English.
XX The invention relates to secreted polypeptide-related proteins and
CC nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The
CC nucleic acids, proteins and antibodies specific to the proteins are
CC useful in screening assays, predictive medicine (e.g. diagnostic assays,
CC prognostic assays, monitoring clinical trials and pharmacogenetics) and
CC prophylactic and therapeutic methods. The sequences are used in
CC diagnosing, preventing or treating proliferative disorders (e.g.
CC cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune
CC disorders (e.g. multiple sclerosis or lupus), neurological disorders
CC (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular
CC disorders (e.g. myocardial infarction or congestive heart disease), blood
CC platelet disorders (e.g. thrombocytopenia or anaemia) and disorders
CC involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic
CC acids may also be used in chromosome mapping, tissue typing and forensic
CC biology, and as surrogate markers. This sequence represents a secreted
CC polypeptide-related cDNA of the invention. Note: The sequence data for
CC this patent was obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html
XX SQ Sequence 2145 BP; 556 A; 561 C; 575 G; 453 T; 0 U; 0 Other;
Query Match 99.7%; Score 1459.8; DB 8; Length 2145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ATGACATCTAAGAATTATCCCGGACCTACCCCAATCACACTGTTTGGGAAAGACAAATT 60
Db 157 ATGACATCTAAGAATTATCCCGGACCTACCCCAATCACACTGTTTGGGAAAGACAAATT 216
Qy 61 ACAGTACCAAGGGGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCAG 120
Db 217 ACAGTACCAAGGGGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCAG 276
Qy 121 ACCTGTGCTTCTGACTATCTTCTTCCACAGCTCTTCAGATCAATATGGTCCATCTGT 180
Db 277 ACCTGTGCTTCTGACTATCTTCTTCCACAGCTCTTCAGATCAATATGGTCCATCTGT 336
Qy 181 GGAAGTATGACTGTTCCTCAAGAACTCTGTTGAACAAGTGAAGTAAACCGTCGGCTTT 240

Db 337 GGAAGTATGACTGTTCCTCAAGAACTCTGTTGAACAACAAGTGAAGTAAACCGTCCGCTTT 396
Qy 241 GAGAGTGGATCCCAATTTCTGGCCGGGTTTTTTTGTCTGACCTATGCGAGCAGCGACCAAT 300
Db 397 GAGAGTGGATCCCAATTTCTGGCCGGGTTTTTTTGTCTGACCTATGCGAGCAGCGACCAAT 456
Qy 301 CAGATTTAATAAATGTTTGAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAAA 360
Db 457 CAGATTTAATAAATGTTTGAACGAGCTAGCCATTATTTGAAGACAGAAATACAGCAAA 516
Qy 361 TTCTGCCAGCTGGTTGTAGAGACGTPAGCAGAGACATTTCTGGGAAATATGGTAGATGA 420
Db 517 TTCTGCCAGCTGGTTGTAGAGACGTPAGCAGAGACATTTCTGGGAAATATGGTAGATGA 576
Qy 421 TATAGAGATACCTCTTTATTTGTGCAAGCTGCCATCCATGCAAGGAATAATTTGCTGATGA 480
Db 577 TATAGAGATACCTCTTTATTTGTGCAAGCTGCCATCCATGCAAGGAATAATTTGCTGATGA 636
Qy 481 CTAGGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATGAAGGATTCG 540
Db 637 CTAGGTGGCCAGATCAGTGTGCTTCAGCGCAAGGGATCAGTCGATATGAAGGATTCG 696
Qy 541 GCCAATGCTGTTCTTTTCGAGGGATGTTCCCTGTGACAGCAAGCGATTTCTGTGTTTACCTCC 600
Db 697 GCCAATGCTGTTCTTTTCGAGGGATGTTCCCTGTGACAGCAAGCGATTTCTGTGTTTACCTCC 756
Qy 601 AATGTTTGACGAGATCCTTTGAGTTTTTGAACCTGACGGGCAATTCAGAGCTTCTTCTCTCA 660
Db 757 AATGTTTGACGAGATCCTTTGAGTTTTTGAACCTGACGGGCAATTCAGAGCTTCTTCTCTCA 816
Qy 661 TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTCACTGCTCTCTGCGCAAGGCCGACATT 720
Db 817 TGGCAGTCGGTCAATGAGAGTGGAGACCAAGTTCACTGCTCTCTGCGCAAGGCCGACATT 876
Qy 721 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACAACAACAACCAACAGAG 780
Db 877 CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACAACAACAACCAACAGAG 936
Qy 781 TGGCTCGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAACAGGATCT 840
Db 937 TGGCTCGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAACAGGATCT 996
Qy 841 ACACAGTCGAATCTCACTTTTATGTTTAAAGTTTGTGATGATCTTCAAAAACAATAAT 900
Db 997 ACAAGTCGAATCTCACTTTTATGTTTAAAGTTTGTGATGATCTTCAAAAACAATAAT 1056
Qy 901 TCTAAGTGAAGACCTATATAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGGTAAAC 960
Db 1057 TCTAAGTGAAGACCTATATAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGGTAAAC 1116
Qy 961 TCTAAGTTCGGGACCCAGTGCAAAAACAATTTCAATCCCTCCCATCTGCGGCGAGATATGTG 1020
Db 1117 TCTAAGTTCGGGACCCAGTGCAAAAACAATTTCAATCCCTCCCATCTGCGGCGAGATATGTG 1176
Qy 1021 CGGGTTGTCCTCCAGACATCGCCACAGAGATAGCTTGAAGTGGAGCTCATTTGGTTGC 1080
Db 1177 CGGGTTGTCCTCCAGACATCGCCACAGAGATAGCTTGAAGTGGAGCTCATTTGGTTGC 1236
Qy 1081 CAGATTACAAAGTAAATGATTTCAATGTTGGGCGCAAGCAAGTCAAAAGCACCAAGTGT 1140
Db 1237 CAGATTACAAAGTAAATGATTTCAATGTTGGGCGCAAGCAAGTCAAAAGCACCAAGTGT 1296
Qy 1141 TCATAAGAAAGAGATGAGACAATCAAGGCCCATTCCTCTCGGAGAAACAATCCACA 1200
Db 1297 TCATAAGAAAGAGATGAGACAATCAAGGCCCATTCCTCTCGGAGAAACAATCCACA 1356
Qy 1201 GGAATAACATTACAAGCGGTGCTATTTCCATTTGCTCTCTGCTGCTGCTGCTGCT 1260
Db 1357 GGAATAACATTACAAGCGGTGCTATTTCCATTTGCTGCTCTCTGCTGCTGCTGCT 1416
Qy 1261 GGAATGGGATCTTTTGCAGCCCTTTAGAAAGAAAGAAAGAAAGGAAAGTCCGTATGGATCA 1320
Db 1417 GGAATGGGATCTTTTGCAGCCCTTTAGAAAGAAAGAAAGAAAGGAAAGTCCGTATGGATCA 1476

QY 1321 GCGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAAATATCCCTTTGCCAGACATCAG 1380
|||
Db 1477 GCAGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAAATATCCCTTTGCCAGACATCAG 1536
|||
QY 1381 TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAGGAGATGACAAAGTTAGATCTC 1440
|||
Db 1537 TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAGGAGATGACAAAGTTAGATCTC 1596
|||
QY 1441 ATCAAGTGTATGGCAGGTTA 1463
|||
Db 1597 ATCAAGTGTATGGCAGGTTA 1619
|||

RESULT 9
ADQ10135
ID ADQ10135 standard; CDNA; 2145 BP.
XX
AC ADQ10135;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human polynucleotide #11.
XX
KW Human; gene; ss; cancer; obesity; gastritis; diarrhoea; haemorrhoid;
KW asthma; anaemia; graft-versus-host reaction; allergic reaction;
KW cystic fibrosis; hypogonadism; cardiovascular disorder; arthritis;
KW osteoarthritis; arteriosclerosis; hypertension; bacterial infection;
KW psoriasis; diabetes mellitus; hepatitis; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; AIDS; tuberculosis;
KW viral infection; malaria; goiter; infertility; endometriosis;
KW muscular disorder.
XX
OS Homo sapiens.
XX
PN US2004121396-A1.
XX
PD 24-JUN-2004.
XX
PF 19-DEC-2003; 2003US-00741790.
XX
PR 14-JUN-1999; 99US-00333159.
PR 29-JUN-1999; 99US-00342364.
PR 10-SEP-1999; 99US-00393996.
PR 19-OCT-1999; 99US-00420707.
PR 07-JAN-2000; 2000US-00479249.
PR 27-APR-2000; 2000US-00559497.
PR 24-MAY-2000; 2000US-00578063.
PR 16-JUN-2000; 2000US-00596194.
PR 23-JUN-2000; 2000US-00602871.
PR 30-JUN-2000; 2000US-00608452.
PR 12-JAN-2001; 2001US-00759130.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
XX
PI Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;
PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl AD;
XX
XX WPI; 2004-479675/45.
XX
PT New TANGO, INTERCEPT, and MANGO, useful in diagnosing, preventing, and
PT treating cancer, constipation, hemorrhoids, cystic fibrosis,
PT hypogonadism, psoriasis, hepatitis, Alzheimer's disease, AIDS,
PT tuberculosis, malaria, goiter, infertility.
XX
PS Claim 2; SEQ ID NO 72; 483pp; English.

XX
CC The invention relates to human polynucleotides and the polypeptides they
CC encode. The invention also relates to a host cell containing a
CC polynucleotide of the invention, an antibody which selectively binds with
CC a polypeptide of the invention, a method of detecting the presence of a
CC polypeptide in a sample, a method of identifying a compound which binds
CC with a polypeptide, and a method of modulating the activity of a

CC polypeptide. The polynucleotides, polypeptides and compositions are
CC useful for diagnosing, preventing and/or treating cancer, obesity,
CC gastritis, diarrhoea, haemorrhoids, asthma, anaemia, graft-versus-host
CC reactions, allergic reactions, cystic fibrosis, hypogonadism,
CC cardiovascular disorders, arthritis, osteoarthritis, arteriosclerosis,
CC hypertension, bacterial infections, psoriasis, diabetes mellitus,
CC hepatitis, Alzheimer's disease, Huntington's disease, Parkinson's
CC disease, AIDS, tuberculosis, viral infections, malaria, goiter,
CC infertility, endometriosis, wounds and muscular disorders. This sequence
CC represents a human polynucleotide of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification but
CC was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 2145 BP; 556 A; 561 C; 575 G; 453 T; 0 U; 0 Other;

Query Match 99.7%; Score 1459.8; DB 12; Length 2145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGACATCTAAGAATTATCCCGGACCTACCCCAATCACACTGTTGCGAAGACAAATT 60
Db 157 ATGACATCTAAGAATTATCCCGGACCTACCCCAATCACACTGTTGCGAAGACAAATT 216
QY 61 ACAGTACCAAGGGGAAAGACTGATTCTGAGGTGGGAGATTGGATATCGAATCCCAG 120
Db 217 ACAGTACCAAGGGGAAAGACTGATTCTGAGGTGGGAGATTGGATATCGAATCCCAG 276
QY 121 ACCTGCTTCTGACTATCTCTTCCACAGCTCTTCAGATCAATATGTTCCATCTGT 180
Db 277 ACCTGCTTCTGACTATCTCTTCCACAGCTCTTCAGATCAATATGTTCCATCTGT 336
QY 181 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTAACACAGTGAAGTAAACCGTCCGCTTT 240
Db 337 GGAAGTATGACTGTTCCCAAGAACTCTTGTGTAACACAGTGAAGTAAACCGTCCGCTTT 396
QY 241 GAGAGTGGATCCCAATTTCTGCGCGGGTTTTTGTGCTACCTATCGAGCAGCGACCAT 300
Db 397 GAGAGTGGATCCCAATTTCTGCGCGGGTTTTTGTGCTACCTATCGAGCAGCGACCAT 456
QY 301 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTGGAAGACAGAAATCAGCAAA 360
Db 457 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTGGAAGACAGAAATCAGCAAA 516
QY 361 TTCTGCCAGCTGTTGTAGAGACGTAGCAGAGACATTTCTGGGAATATGGTAGATGA 420
Db 517 TTCTGCCAGCTGTTGTAGAGACGTAGCAGAGACATTTCTGGGAATATGGTAGATGA 576
QY 421 TATAGAGATACCTCTTTATTGTGCAAGCTGCCATCCATGCAGGAATAATTTGCTGATGA 480
Db 577 TATAGAGATACCTCTTTATTGTGCAAGCTGCCATCCATGCAGGAATAATTTGCTGATGA 636
QY 481 CTAGTGGCCAGATCAGTGTGCTTCAGCCAAAGGATCAGTCGATATGAAGGATCTTG 540
Db 637 CTAGTGGCCAGATCAGTGTGCTTCAGCCAAAGGATCAGTCGATATGAAGGATCTTG 696
QY 541 GCCAATGTTGTTCTTTTCAGAGGATGTTCCCTGTGACAGAACGATTTCTGTTTACTCC 600
Db 697 GCCAATGTTGTTCTTTTCAGAGGATGTTCCCTGTGACAGAACGATTTCTGTTTACTCC 756
QY 601 AATGTTGACAGATCCTTTGAGTTTGAACCTGACGGGCAATCAGAGCTTCTTCTCA 660
Db 757 AATGTTGACAGATCCTTTGAGTTTGAACCTGACGGGCAATCAGAGCTTCTTCTCA 816
QY 661 TGGCAGTCCGTCAATGAGATGAGACCAAGTTCTCTGCTGCGCCAGCCGACTT 720
Db 817 TGGCAGTCCGTCAATGAGATGAGACCAAGTTCTCTGCTGCGCCAGCCGACTT 876
QY 721 CAGGACCAAGGCCCATCATGCGCTTCGGCGCAGTAGCAACAACCAAAACCAGAGAG 780
Db 877 CAGGACCAAGGCCCATCATGCGCTTCGGCGCAGTAGCAACAACCAAAACCAGAGAG 936
QY 781 TGGCTGGAGATCGATTTTGGGGGAGAAAAAGAAATTAACAGGAATTAGGACCAAGGATCT 840

Db 937 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACACAGGATCT 996
Qy 841 ACACAGTCGAACCTTCAACTTTTATGTTTAAAGAGTTTGTGTGATGAACCTTCAAAAACAATAAT 900
Db 997 ACACAGTCGAACCTTCAACTTTTATGTTTAAAGAGTTTGTGTGATGAACCTTCAAAAACAATAAT 1056
Qy 901 TCTAAGTGGAGACCTTATAAGGAATTTGTAATAAGAAAAGGTGTTTTCAGGGTTAAC 960
Db 1057 TCTAAGTGGAGACCTTATAAGGAATTTGTAATAAGAAAAGGTGTTTTCAGGGTTAAC 1116
Qy 961 TCTAAGTGGAGACCTTATAAGGAATTTGTAATAAGAAAAGGTGTTTTCAGGGTTAAC 1020
Db 1117 TCTAAGTGGAGACCTTATAAGGAATTTGTAATAAGAAAAGGTGTTTTCAGGGTTAAC 1176
Qy 1021 CGGTTGTGTCGCCAGACATGCGACAGAGATAGCCTTTGAAGGTGGAGCTCATTTGGTTGC 1080
Db 1177 CGGTTGTGTCGCCAGACATGCGACAGAGATAGCCTTTGAAGGTGGAGCTCATTTGGTTGC 1236
Qy 1081 CAGATTACACAGGTAAATGATTTCAATTTGTTGGCGCAAGACAAGTCAAAAGCACAGTGTT 1140
Db 1237 CAGATTACACAGGTAAATGATTTCAATTTGTTGGCGCAAGACAAGTCAAAAGCACAGTGTT 1296
Qy 1141 TCAACTAAGAAAAGAGATGAGACATCAACAGGCCATCCCTCGGAGAAACATCCACA 1200
Db 1297 TCAACTAAGAAAAGAGATGAGACATCAACAGGCCATCCCTCGGAGAAACATCCACA 1356
Qy 1201 GGAATAAATTTACACAGGTGGCTTATTCATTTGTTGCTCTCTTGTGCTGCTGTTGCT 1260
Db 1357 GGAATAAATTTACACAGGTGGCTTATTCATTTGTTGCTCTCTTGTGCTGCTGTTGCT 1416
Qy 1261 GGAATGGGATCTTTGACGCTTTTGAAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1320
Db 1417 GGAATGGGATCTTTGACGCTTTTGAAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1476
Qy 1321 GCGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAATAATCCCTTCCAGACATCAG 1380
Db 1477 GCGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAATAATCCCTTCCAGACATCAG 1536
Qy 1381 TCAGCTCAGTTTACCATCAGCTATGATAATGAGAAAGAGATGACACAAAAGTTAGATCTC 1440
Db 1537 TCAGCTCAGTTTACCATCAGCTATGATAATGAGAAAGAGATGACACAAAAGTTAGATCTC 1596
Qy 1441 ATCAAAAGTGATGGCAGTTA 1463
Db 1597 ATCAAAAGTGATGGCAGTTA 1619

RESULT 10

AD128055
ID AD128055 standard; cDNA; 2888 BP.

XX AC AD128055;

XX 15-APR-2004 (first entry)

XX ECNCAD gene clone 184661CB1.

XX ds; gene; nontropic; antisickling; antianemic; antitumor; anti-HIV;
XX anti-allergic; antianemic; antiasthmatic; immunosuppressive;
XX antiatherosclerotic; dermatological; nephrotrophic; antigout;
XX antithyroid; neuroprotective; osteopathic; antipsoriatic; antirheumatic;
XX antiarthritic; antipulser; antinflamatory; ophthalmological;
XX anticonvulsant; antiparkinsonian; antibacterial; virucide; tranquilizer;
XX neuroleptic; antidiabetic; cyostatic; hepatotrophic; gene therapy;
XX human extracellular matrix and cell adhesion molecule; ECNCAD; diagnosis;
XX genetic disorder; adrenoleukodystrophy; Down's syndrome; cystic fibrosis;
XX Gaucher's disease; myotonic dystrophy; sickle cell anemia; thalassemia;
XX Wilms' tumor; immunological disorder; acquired immunodeficiency syndrome;
XX AIDS; adult respiratory distress syndrome; allergy; anemia; asthma;
XX atherosclerosis; autoimmune hemolytic anemia; contact dermatitis;
XX Goodpasture's syndrome; gout; Grave's disease; multiple sclerosis;
XX osteoporosis; psoriasis; rheumatoid arthritis; scleroderma;

KW systemic lupus erythematosus; ulcerative colitis; uveitis;
KW neurological disorder; epilepsy; stroke; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; multiple sclerosis;
KW meningitis; periodic paralysis; mental disorder; mood; anxiety;
KW schizophrenia; amnesia; diabetic neuropathy; connective tissue disorder;
KW osteoporosis; Paget's disease; osteonecrosis; osteomyelitis;
KW chondrosarcoma; giant cell tumor; psoriatic arthritis;
KW infectious arthritis; systemic sclerosis; cell proliferative disorder;
KW actinic keratosis; atherosclerosis; hepatitis; psoriasis; cancer;
KW adenocarcinoma; leukemia; lymphoma; melanoma; myeloma.

XX Homo sapiens.

OS WO200202634-A2.

PN 10-JAN-2002.

XX 29-JUN-2001; 2001WO-US021067.

XX 30-JUN-2000; 2000US-0215454P.

PR 18-JUL-2000; 2000US-0219462P.

PR 12-OCT-2000; 2000US-0240106P.

PR 12-OCT-2000; 2000US-0240111P.

PR 27-OCT-2000; 2000US-0244021P.

PR 14-NOV-2000; 2000US-0248887P.

PR 16-NOV-2000; 2000US-0249570P.

XX (INCY-) INCYTE GENOMICS INC.

XX Tang YT, Yue H, Azinzai Y, He A, Batra S, Lo TP, Nguyen DB;

XX Burdill JD, Marcus GA, Zingler KA, Gandhi AR, Lal P, Kearney L;

XX Burford N, Yao MG, Walla NK, Elliot VS, Patterson C, Khan FA;

XX Baughn MR, Hafalla AJA, Policky JL, Au-Young J, Lu Y, Borowsky ML;

XX Lu DAM, Rankumar J, Yang J, Gururajan R, Warren BA, Gietzen K;

XX Xu Y, Kallikar DA, Lee EA, Thangavelu K, Deleage AM, Lee S;

XX WPI; 2002-154732/20.

XX P-PSDB; ADI28019.

XX Novel isolated human extracellular matrix and cell adhesion molecules

XX useful for treating, preventing connective tissue disorder e.g.

XX osteoporosis, Paget's disease, genetic disorder e.g. cystic fibrosis,

XX thalassemia.

XX Claim 11; SEQ ID NO 47; 270pp; English.

XX The invention relates to a novel isolated human extracellular matrix and

XX cell adhesion molecule (referred to as ECNCAD 1-36), its biologically

XX active or immunogenic fragment or a sequence comprising 90 % identity to

XX ECNCAD 1-36. The molecule is useful for screening a compound for

XX effectiveness as agonist or antagonist of itself. The protein and its

XX encoding nucleic acid are useful in the diagnosis, treatment and

XX prevention of genetic disorder such as adrenoleukodystrophy, Down's

XX syndrome, cystic fibrosis, Gaucher's disease, myotonic dystrophy, sickle

XX cell anemia, thalassemia, Wilms' tumor, etc, immunological disorders such

XX as acquired immunodeficiency syndrome (AIDS), adult respiratory distress

XX syndrome, allergies, anemia, asthma, atherosclerosis, autoimmune

XX hemolytic anemia, contact dermatitis, Goodpasture's syndrome, gout,

XX Grave's disease, multiple sclerosis, osteoporosis, ulcerative colitis,

XX arthritis, scleroderma, systemic lupus erythematosus, epidermal colitis,

XX uveitis, etc, a neurological disorder such as epilepsy, stroke,

XX Alzheimer's disease, Huntington's disease, Parkinson's disease, multiple

XX sclerosis, bacterial and viral meningitis, periodic paralysis, mental

XX disorders including mood, anxiety, and schizophrenic disorders, amnesia,

XX diabetic neuropathy, etc, connective tissue disorder such as

XX osteoporosis, Paget's disease, osteonecrosis, osteomyelitis,

XX chondrosarcoma, giant cell tumor, psoriatic arthritis, infectious

XX arthritis, systemic sclerosis, etc, and a cell proliferative disorder

XX such as actinic keratosis, atherosclerosis, hepatitis, psoriasis, cancers

XX including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, etc.

XX This sequence represents the cDNA sequence encoding one of the novel

XX proteins.

SQ Sequence 2888 BP; 736 A; 696 C; 775 G; 681 T; 0 U; 0 Other;									
Query Match 99.7%; Score 1459.8; DB 6; Length 2888;									
Best Local Similarity 99.9%; Pred. No. 0;									
Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY	1	ATGACATCTAAGAAATTATCCGGGACCTACCCCAATCACACTGTTTGCAGAAAGACAAATT	60						
DB	282	ATGACATCTAAGAAATTATCCGGGACCTACCCCAATCACACTGTTTGGGAAAGACAAATT	341						
QY	61	ACAGTACCAAGGGGAAAGACATGATCTGAGGTGGGAGATTGGATATCGAATCCAG	120						
DB	342	ACAGTACCAAGGGGAAAGACATGATCTGAGGTGGGAGATTGGATATCGAATCCAG	401						
QY	121	ACCTGTGCTTCTGACTATCTTCTTCCACAGCTCTTTCAGATCAATATGCTCCATCTGT	180						
DB	402	ACCTGTGCTTCTGACTATCTTCTTCCACAGCTCTTTCAGATCAATATGCTCCATCTGT	461						
QY	181	GGAAATATGACTGTTCCCAAGAACTCTTGTGGAACAACAGTGAAGTAAACCGTCCGCTTT	240						
DB	462	GGAAATATGACTGTTCCCAAGAACTCTTGTGGAACAACAGTGAAGTAAACCGTCCGCTTT	521						
QY	241	GAGAGTGGATCCACATTTCTGCGGGGTTTTTGTGCTGACCTATGGAGCAGCGACCAT	300						
DB	522	GAGAGTGGATCCACATTTCTGCGGGGTTTTTGTGCTGACCTATGGAGCAGCGACCAT	581						
QY	301	CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTTGAAGACAGAAATACAGCAA	360						
DB	582	CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTTTGAAGACAGAAATACAGCAA	641						
QY	361	TTCTGCCCCAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGTGA	420						
DB	642	TTCTGCCCCAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGTGA	701						
QY	421	TATAGATACCTCTTTATTTGCGAAAGCTGCCATCCATCGACGAATAATTGCTGATGAA	480						
DB	702	TATAGATACCTCTTTATTTGCGAAAGCTGCCATCCATCGACGAATAATTGCTGATGAA	761						
QY	481	CTAGGTGGCCAGATCAGTGTCTTACGCGCAAGAGGATCAGTCGATGAAGGATTCG	540						
DB	762	CTAGGTGGCCAGATCAGTGTCTTACGCGCAAGAGGATCAGTCGATGAAGGATTCG	821						
QY	541	GCCAAATGGTGTCTTTTCGAGGGATGGTTCCTGTCCAGACAAGCGATTTCTGTTTACCTCC	600						
DB	822	GCCAAATGGTGTCTTTTCGAGGGATGGTTCCTGTCCAGACAAGCGATTTCTGTTTACCTCC	881						
QY	601	AATGTTGACAGAGATCTTGTAGTTTGAACCTGACGGGCAATCAGAGCTTCTCCTCA	660						
DB	882	AATGTTGACAGAGATCTTGTAGTTTGAACCTGACGGGCAATCAGAGCTTCTCCTCA	941						
QY	661	TGGCAGTCCGTCAATCAGAGTGGAGACCAAGTTTCACTGGTCTCTGGCCAAAGCCGACTT	720						
DB	942	TGGCAGTCCGTCAATCAGAGTGGAGACCAAGTTTCACTGGTCTCTGGCCAAAGCCGACTT	1001						
QY	721	CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACACCAACCAACCCAGAG	780						
DB	1002	CAGGACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACACCAACCAACCCAGAG	1061						
QY	781	TGGCTCGAGATCGATTTGGGGGAGAAAAGAAATAACAGGAATTAAGGACCAAGATCT	840						
DB	1062	TGGCTCGAGATCGATTTGGGGGAGAAAAGAAATAACAGGAATTAAGGACCAAGATCT	1121						
QY	841	ACACAGTCCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAACATAT	900						
DB	1122	ACACAGTCCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAACCTTCAAAACATAT	1181						
QY	901	TCTAAGTGAAGACCTATAAGGAATTGTGAATAATCAAGAAAGGTGTTTCAGGGTAAC	960						
DB	1182	TCTAAGTGAAGACCTATAAGGAATTGTGAATAATCAAGAAAGGTGTTTCAGGGTAAC	1241						
QY	961	TCTAAGTTCGGGACCCAGTGCAGAAACAAATTTTCATCCCTCCCATCGTGGCCAGATATG	1020						
DB	1242	TCTAAGTTCGGGACCCAGTGCAGAAACAAATTTTCATCCCTCCCATCGTGGCCAGATATG	1301						

RESULT 11

ID	ABN86493
XX	ABN86493 standard; cDNA; 3151 BP.
AC	ABN86493;
XX	
DT	21-OCT-2002 (first entry)
XX	
DE	Human neurophilin homologue polypeptide, zcub5 encoding cDNA.
XX	
KW	Neurophilin; zcub5; human; antitumour; antidiabetic; ophthalmological;
KW	antiatherosclerotic; antipsoriatic; antirheumatic; antithrombotic; gene;
KW	cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
XX	cytostatic; gene therapy; ss.
OS	Homo sapiens.
XX	
PH	Key
CDS	Location/Qualifiers
FT	76..2223
FT	/*tag= a
FT	/product= "zcub5"
XX	
PN	WO200253739-A2.
XX	
PD	11-JUL-2002.
XX	
PF	15-NOV-2001; 2001WO-US045542.
XX	
PR	15-NOV-2000; 2000US-0249004P.
XX	
PA	(ZYMO) ZYMOGENETICS INC.
XX	
PI	Fox BA, Gao Z, Shoemaker KE;
XX	
DR	WPI; 2002-590634/63.
DR	P-PSDB; ABB81000.
XX	
PT	Novel isolated neurophilin homolog polypeptide, termed zcub5, useful in
PT	diagnosis or treatment of disorders associated with abnormal cell

PT proliferation such as cancer and diseases of the nervous system.

XX Example 2; Page 72-77; 101pp; English.

XX The invention relates to an isolated neurophilin homologue polypeptide, termed zcub5. The polypeptide can be expressed by standard recombinant methodology. The zcub5 polypeptide and polynucleotide are useful in a variety of therapeutic, diagnostic and research applications. The polypeptide is useful for producing antibodies, for imaging tumours or other sites of abnormal cell proliferation, for treating solid tumours, retinopathies (including diabetic retinopathy and macular degeneration), atherosclerosis, psoriasis, rheumatoid arthritis and growth factor-dependent pathologies, to design agonists and antagonists of neurophilin -semaphorin interactions, for repairing neurological damage due to stroke, head and spinal injuries, for treating neurodegenerative diseases such as multiple sclerosis, Alzheimer's disease, and Parkinson's disease, for mediating development and innervation of stomach tissue, for identifying, labeling, and isolating selected cell types, as a target for cell-specific delivery of diagnostic and therapeutic agent, and to identify inhibitor of zcub5 activity. The zcub5 polypeptide, polynucleotide and modulators are useful in diagnosis or treatment of disorders associated with abnormal cell proliferation, including cancer, impaired or excessive vasculogenesis or angiogenesis and diseases of the nervous system. The present sequence represents a cDNA encoding the human zcub5 polypeptide

XX Sequence 3151 BP; 832 A; 752 C; 824 G; 743 T; 0 U; 0 Other;

Query Match	99.78;	Score 1459.8;	DB 6;	Length 3151;
Best Local Similarity	99.99;	Pred. No. 0;		
Matches 1461;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	ATGACATCTAAGAAATTATCCGGGACCTACCCCAATCACACTGTTTCGGAAGACAATT	60	
DB	232	ATGACATCTAAGAAATTATCCGGGACCTACCCCAATCACACTGTTTCGGAAGACAATT	291	
QY	61	ACAGTACCAAGGGGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCAG	120	
DB	292	ACAGTACCAAGGGGAAAGACTGATCTGAGGTTGGGAGATTGGATATCGAATCCAG	351	
QY	121	ACCTGTGCTCTGACTATCTCTCTCCAGCTCTTCAGATCAATATGTCCTATCTGT	180	
DB	352	ACCTGTGCTCTGACTATCTCTCTCCAGCTCTTCAGATCAATATGTCCTATCTGT	411	
QY	181	GGAAGTATGACTGTTCCCAAGAACTCTGTTGAACACAGTGAAGTAAACCGTCCGCTTT	240	
DB	412	GGAAGTATGACTGTTCCCAAGAACTCTGTTGAACACAGTGAAGTAAACCGTCCGCTTT	471	
QY	241	GAGAGTGATCCCAATTTCTGGCGGGGTTTTTTTGTGACCTATGCGAGCGACCAT	300	
DB	472	GAGAGTGATCCCAATTTCTGGCGGGGTTTTTTTGTGACCTATGCGAGCGACCAT	531	
QY	301	CCAGATTTAATACATGTTTGGACGAGCTAGCCATTTATTTGAAGACAGATACAGCAA	360	
DB	532	CCAGATTTAATACATGTTTGGACGAGCTAGCCATTTATTTGAAGACAGATACAGCAA	591	
QY	361	TTCTGCCAGCTGGTTGTAGAGAGCTAGCAGGAGACATTTCTGGGAATATGTTAGATGGA	420	
DB	592	TTCTGCCAGCTGGTTGTAGAGAGCTAGCAGGAGACATTTCTGGGAATATGTTAGATGGA	651	
QY	421	TATAGAGATACCTCTTTTATTTGGAAAGCTGCGATCCCATCGCATATGCGATGAA	480	
DB	652	TATAGAGATACCTCTTTTATTTGGAAAGCTGCGATCCCATCGCATATGCGATGAA	711	
QY	481	CTAGGTGCGCAGATCAGTGTCTCTCAGCGCAAGGGATCAGTCGATATGAGGGATCTGT	540	
DB	712	CTAGGTGCGCAGATCAGTGTCTCTCAGCGCAAGGGATCAGTCGATATGAGGGATCTGT	771	
QY	541	GCCAAATGGTGTCTTTCTGAGGGATGGTTCCCTGTGTCAGACAAAGCGATTTCTGTTTACCTCC	600	
DB	772	GCCAAATGGTGTCTTTCTGAGGGATGGTTCCCTGTGTCAGACAAAGCGATTTCTGTTTACCTCC	831	
QY	601	AATGGTTGCAGACATCCTTGAGTGTGTAACCTGACGGGCAATCAGACGCTCTTCTCTCA	660	

DB	832	AATGGTTGCAGCAGATCTCTTGAACCTTGACGGGCAATCAGAGCTTCTTCTCTCA	891	
QY	661	TGGCAGTCCGTCAATGAGAGTGGAGACCAAGTTTCACTGGTCTCTCTGGCCAAAGCCGACTT	720	
DB	892	TGGCAGTCCGTCAATGAGAGTGGAGACCAAGTTTCACTGGTCTCTCTGGCCAAAGCCGACTT	951	
QY	721	CAGGACCAAGGCCCATCATATGGGCTTCGGGCGCAGTAGCAACCAACCAAAACCCAGAGAG	780	
DB	952	CAGGACCAAGGCCCATCATATGGGCTTCGGGCGCAGTAGCAACCAACCAAAACCCAGAGAG	1011	
QY	781	TGGCTGGAGATCGATTTGGGGGAGAAAGAAATAACAGGAATTAAGGACCAAGATCT	840	
DB	1012	TGGCTGGAGATCGATTTGGGGGAGAAAGAAATAACAGGAATTAAGGACCAAGATCT	1071	
QY	841	ACACAGTCCGAATCTTCAACTTTTATGTAAAGAGTTTGTGATGAATTTCAAAAAAATAAT	900	
DB	1072	ACACAGTCCGAATCTTCAACTTTTATGTAAAGAGTTTGTGATGAATTTCAAAAAAATAAT	1131	
QY	901	TCTAAGTGAAGACCTTATAAGGAATTTGAATAATGAAGAAAGGTGTTTCAAGGTAAC	960	
DB	1132	TCTAAGTGAAGACCTTATAAGGAATTTGAATAATGAAGAAAGGTGTTTCAAGGTAAC	1191	
QY	961	TCTAATCTTTCGGGACCCAGTGCAGAAATTTTCATCCCTCCCATCTGTCGCGACAGATGTG	1020	
DB	1192	TCTAATCTTTCGGGACCCAGTGCAGAAATTTTCATCCCTCCCATCTGTCGCGACAGATGTG	1251	
QY	1021	CGGGTTGTCCCCCAGACATGGCCACAGAGATAGCCTTGAAGGTGGAGCTCATTTGGTTGC	1080	
DB	1252	CGGGTTGTCCCCCAGACATGGCCACAGAGATAGCCTTGAAGGTGGAGCTCATTTGGTTGC	1311	
QY	1081	CAGATTACAAAGGTAAATGATTCATTTGTTGTCGCGCAAGCAAGTCAAAAGCACAGTGT	1140	
DB	1312	CAGATTACAAAGGTAAATGATTCATTTGTTGTCGCGCAAGCAAGTCAAAAGCACAGTGT	1371	
QY	1141	TCAACTTAAGAAAGAGTGAACAATCACAAGGCCCATCCCTCGGAAGAAACATCCACA	1200	
DB	1372	TCAACTTAAGAAAGAGTGAACAATCACAAGGCCCATCCCTCGGAAGAAACATCCACA	1431	
QY	1201	GGAATAAACATTACAACGGTGGCTATTTCATTTGGTGTCTCTTGTCTGGTGTGTTGCT	1260	
DB	1432	GGAATAAACATTACAACGGTGGCTATTTCATTTGGTGTCTCTTGTCTGGTGTGTTGCT	1491	
QY	1261	GGAATGGGATCTTTGCGAGCTTTAGAAAGAAAGAAAGAAAGTCCGTATGATCA	1320	
DB	1492	GGAATGGGATCTTTGCGAGCTTTAGAAAGAAAGAAAGAAAGTCCGTATGATCA	1551	
QY	1321	GCGGAGGCTCAGAAACAGACTGTGGAAGCAGATTAAATATCCCTTTGCGACACATCAG	1380	
DB	1552	GCGGAGGCTCAGAAACAGACTGTGGAAGCAGATTAAATATCCCTTTGCGACACATCAG	1611	
QY	1381	TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAAGGAGATGACACAAAAAGTTAGATCTC	1440	
DB	1612	TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAAGGAGATGACACAAAAAGTTAGATCTC	1671	
QY	1441	ATCACAAGTGAATGGCAGGTTA	1463	
DB	1672	ATCACAAGTGAATGGCAGGTTA	1694	

RESULT 12

AAS00660

ID AAS00660 standard; cDNA; 3594 BP.

XX AAS00660;

XX AC

XX 07-SEP-2001 (first entry)

XX DT

XX Human TANGO 229 cDNA.

XX DB

XX Human; TANGO 229; T cell; heart; liver; pancreas; placenta; brain; lung;

XX skeletal muscle; kidney; spleen; lymph node; peripheral blood leukocyte;

XX bone marrow; thymus tissue; abnormal blood coagulation; asthma; cancer;

anaphylaxis; hepatitis; multiple sclerosis; coronary artery disease; ss;
malaria; atopic dermatitis; amyotrophic lateral sclerosis; meningitis;
attention deficit disorder; Crohn's disease; gastroenteritis; goitre;
hypoglycaemia; diabetes mellitus; endometriosis; pulmonary embolism;
muscular dystrophy; immuno-competence; vertebrae; blood; serum.

Homo sapiens.

Key Location/Qualifiers

CDS 72..2219

/*tag= a

/product= "Human TANGO 229"

72..173

/*tag= b

174..2216

/*tag= c

/product= "Mature human TANGO 229"

W0200129088-AL.

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anaphylaxis; hepatitis; multiple sclerosis; coronary artery disease; ss;
malaria; atopic dermatitis; amyotrophic lateral sclerosis; meningitis;
attention deficit disorder; Crohn's disease; gastroenteritis; goitre;
hypoglycaemia; diabetes mellitus; endometriosis; pulmonary embolism;
muscular dystrophy; immuno-competence; vertebrae; blood; serum.

Homo sapiens.

Key Location/Qualifiers

CDS 72..2219

/*tag= a

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72..173

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/*tag= c

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anaphylaxis; hepatitis; multiple sclerosis; coronary artery disease; ss;
malaria; atopic dermatitis; amyotrophic lateral sclerosis; meningitis;
attention deficit disorder; Crohn's disease; gastroenteritis; goitre;
hypoglycaemia; diabetes mellitus; endometriosis; pulmonary embolism;
muscular dystrophy; immuno-competence; vertebrae; blood; serum.

Homo sapiens.

Key Location/Qualifiers

CDS 72..2219

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72..173

/*tag= b

174..2216

/*tag= c

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anaphylaxis; hepatitis; multiple sclerosis; coronary artery disease; ss;
malaria; atopic dermatitis; amyotrophic lateral sclerosis; meningitis;
attention deficit disorder; Crohn's disease; gastroenteritis; goitre;
hypoglycaemia; diabetes mellitus; endometriosis; pulmonary embolism;
muscular dystrophy; immuno-competence; vertebrae; blood; serum.

Homo sapiens.

Key Location/Qualifiers

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/*tag= a

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W0200129088-AL.

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anaphylaxis; hepatitis; multiple sclerosis; coronary artery disease; ss;
malaria; atopic dermatitis; amyotrophic lateral sclerosis; meningitis;
attention deficit disorder; Crohn's disease; gastroenteritis; goitre;
hypoglycaemia; diabetes mellitus; endometriosis; pulmonary embolism;
muscular dystrophy; immuno-competence; vertebrae; blood; serum.

Homo sapiens.

Key Location/Qualifiers

CDS 72..2219

/*tag= a

/product= "Human TANGO 229"

72..173

/*tag= b

174..2216

/*tag= c

/product= "Mature human TANGO 229"

W0200129088-AL.

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Qy 1261 GGAATGGGATCTTTGAGCCTTTAGAAAAGAAAGAAAGAAAGTCCGTATGATCA 1320
 Db 1488 GGAATGGGATCTTTGAGCCTTTAGAAAAGAAAGAAAGAAAGTCCGTATGATCA 1547
 Qy 1321 GCGAGGCTCAGAAAACAGACTGTTGGAACGAGTTAAATATCCCTTGGCAGATCAG 1380
 Db 1548 GCGAGGCTCAGAAAACAGACTGTTGGAACGAGTTAAATATCCCTTGGCAGATCAG 1607
 Qy 1381 TCAGCTGAGTTTACCATCAGCTATGATAATGAGAGGAGATGACACAAAAAGTTAGATCTC 1440
 Db 1608 TCAGCTGAGTTTACCATCAGCTATGATAATGAGAGGAGATGACACAAAAAGTTAGATCTC 1667
 Qy 1441 ATCACAAGTATGATGGCAGTTA 1463
 Db 1668 ATCACAAGTATGATGGCAGATTA 1690

RESULT 13

ACD66717

ID ACD66717 standard; cDNA; 3594 BP.

XX AC ACD66717;

XX AC ACD66717;

XX DT 17-SEP-2003 (first entry)

XX DE

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PT TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or treating disorders such as cancer, diabetes or atherosclerosis, and in forensic biology.

PS Claim 2; Fig 10A-10F; 482pp; English.

XX The invention relates to secreted polypeptide-related proteins and CC nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The CC nucleic acids, proteins and antibodies specific to the proteins are CC useful in screening assays, predictive medicine (e.g. diagnostic assays, CC prognostic assays, monitoring clinical trials and pharmacogenetics) and CC prophylactic and therapeutic methods. The sequences are used in CC diagnosing, preventing or treating proliferative disorders (e.g. CC cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune CC disorders (e.g. multiple sclerosis or lupus), neurological disorders CC (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular CC disorders (e.g. myocardial infarction or congestive heart disease), blood CC platelet disorders (e.g. thrombocytopenia or anaemia) and disorders CC involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic CC acids may also be used in chromosome mapping, tissue typing and forensic CC biology, and as surrogate markers. This sequence represents a secreted CC polypeptide-related cDNA of the invention. Note: The sequence data for CC this patent was obtained in electronic format directly from USPTO at CC seqdata.uspto.gov/sequence.html

XX SQ Sequence 3594 BP; 958 A; 810 C; 921 G; 905 T; 0 U; 0 Other;

Query Match 99.7%; Score 1459.8; DB 8; Length 3594;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGACATCTAAGAAATATATCCCGGACCTACCCCAATCACACTGTTTCGAAAAGACAATT 60
 Db 228 ATGACATCTAAGAAATATATCCCGGACCTACCCCAATCACACTGTTTCGAAAAGACAATT 287
 Qy 61 ACAGTACCAGGAGGAGAAAGACTGATCTGAGGTGGAGATTGGATATCGAATCCAG 120
 Db 288 ACAGTACCAGGAGGAGAAAGACTGATCTGAGGTGGAGATTGGATATCGAATCCAG 347
 Qy 121 ACCTGTGCTTCTGACTATCTTCTTCCACAGCTCTTCCAGATCAATATGTCATCTGT 180
 Db 348 ACCTGTGCTTCTGACTATCTTCTTCCACAGCTCTTCCAGATCAATATGTCATCTGT 407
 Qy 181 GGAAGTATGACTGTTTCCAAAAGAACTCTTGTGAAACAAAGTGAAGTAAACCGTCGCTTT 240
 Db 408 GGAAGTATGACTGTTTCCAAAAGAACTCTTGTGAAACAAAGTGAAGTAAACCGTCGCTTT 467
 Qy 241 GAGAGTGGATCCACATTTCTGCGCGGGTCTTGTGCTGACCTATGCGAGCAGGACCAT 300
 Db 468 GAGAGTGGATCCACATTTCTGCGCGGGTCTTGTGCTGACCTATGCGAGCAGGACCAT 527
 Qy 301 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTTGAAGCAGAAATACAGCAA 360
 Db 528 CCAGATTTAATAACATGTTTGGAAACGAGCTAGCCATTATTTGAAGCAGAAATACAGCAA 587
 Qy 361 TTCTGCCCCAGCTGTTGTAGAGACGTAGAGAGACATTTCTGGGAATATGTTAGATGGA 420
 Db 588 TTCTGCCCCAGCTGTTGTAGAGACGTAGAGAGACATTTCTGGGAATATGTTAGATGGA 647
 Qy 421 TATAGAGATACCTCTTTTATTTGTCAAAGCTGCCATCCATGAGGAATAATTTGCTGATGAA 480
 Db 648 TATAGAGATACCTCTTTTATTTGTCAAAGCTGCCATCCATGAGGAATAATTTGCTGATGAA 707
 Qy 481 CTAGGTGGCCAGATCAGTGTCTTTCAGCGCAAGGAGATCAGTGCATATGAAGGATTCGT 540
 Db 708 CTAGGTGGCCAGATCAGTGTCTTTCAGCGCAAGGAGATCAGTGCATATGAAGGATTCGT 767
 Qy 541 GCCAATGCTGTTCTTTCAGGGATGGTTCCTGTCCAGCAGAGCATTTCTGTTTACCTCC 600
 Db 768 GCCAATGCTGTTCTTTCAGGGATGGTTCCTGTCCAGCAGAGCATTTCTGTTTACCTCC 827
 Qy 601 AATGGTTGCAGCAGATCCTTTGAGTTTGAACCTTGACCGGCAAAATCAGAGCTTCTTCTCA 660

PI New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,

Db 828 AATGGTTGCAGCAGATCCTTGGAGTTTGAACCTGACGGGCAAAATCAGAGCTTCTTCTCTCA 887
Qy 661 TGGCAGTCGTCATGAGAGTGGAGACCAAGTTTCACTGGTCTCTTGGCCCAAGCCGACTT 720
Db 888 TGGCAGTCGTCATGAGAGTGGAGACCAAGTTTCACTGGTCTCTTGGCCCAAGCCGACTT 947
Qy 721 CAGGACCAAGCCCATCATGGCTTCGGGGGACAGTAGCAACCAACCAACCAACCAAGAG 780
Db 948 CAGGACCAAGCCCATCATGGCTTCGGGGGACAGTAGCAACCAACCAACCAACCAAGAG 1007
Qy 781 TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAATAACAGGAATTAGGACCAAGATCT 840
Db 1008 TGGCTGGAGATCGATTTGGGGGAGAAAAAGAAATAACAGGAATTAGGACCAAGATCT 1067
Qy 841 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTTCGTGATGAACCTTCAAAAACAATAAT 900
Db 1068 ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTTCGTGATGAACCTTCAAAAACAATAAT 1127
Qy 901 TCTAAGTGGAGACCTATAAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGGTAAC 960
Db 1128 TCTAAGTGGAGACCTATAAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGGTAAC 1187
Qy 961 TCTAAGTGGAGACCTATAAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGGTAAC 1020
Db 1188 TCTAAGTGGAGACCTATAAAGGAATTTGTAATAATGAAGAAAGGTGTTTCAGGGTAAC 1247
Qy 1021 CGGGTTGTCCCGCAGACATGCGACCGAGGATAGCCTTGAAGGTGGAGCTCATTTGGTTGC 1080
Db 1248 CGGGTTGTCCCGCAGACATGCGACCGAGGATAGCCTTGAAGGTGGAGCTCATTTGGTTGC 1307
Qy 1081 CAGATTACACAAGGTAATGATTCATTTGGTGTGGCGCAAGACAAAGTCAAAAGCACCAGTGTT 1140
Db 1308 CAGATTACACAAGGTAATGATTCATTTGGTGTGGCGCAAGACAAAGTCAAAAGCACCAGTGTT 1367
Qy 1141 TCAACTAAGAAAGAGATGAGACAATCAAGGCCCATCCCTCGGAAGAAATCCACACA 1200
Db 1368 TCAACTAAGAAAGAGATGAGACAATCAAGGCCCATCCCTCGGAAGAAATCCACACA 1427
Qy 1201 GGAATAAACATTACACGGTGGCTATTCCATTCGTGCTCTCTGTCCTGCTGTTGCT 1260
Db 1428 GGAATAAACATTACACGGTGGCTATTCCATTCGTGCTCTCTGTCCTGCTGTTGCT 1487
Qy 1261 GGAATGGGATCTTTGAGAGCTTTAGAAAGAAAGAAAGAAAGTCCGTATGGATCA 1320
Db 1488 GGAATGGGATCTTTGAGAGCTTTAGAAAGAAAGAAAGTCCGTATGGATCA 1547
Qy 1321 GCGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAATATATCCCTTTGCGCAGATCAG 1380
Db 1548 GCGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTAATATATCCCTTTGCGCAGATCAG 1607
Qy 1381 TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAAGGAGATGACACAAAGTTAGATCTC 1440
Db 1608 TCAGCTGAGTTTACCATCAGCTATGATTAATGAGAAGGAGATGACACAAAGTTAGATCTC 1667
Qy 1441 ATCAAGTGTATGGCAGGTTA 1463
Db 1668 ATCAAGTGTATGGCAGGTTA 1690

RESULT 14

ADQ10134

ID ADQ10134 standard; cdna; 3594 BP.

XX AC ADQ10134;

XX AC ADQ10134;

XX AC ADQ10134;

DT 09-SEP-2004 (first entry)

DE Human polynucleotide #10.

XX Human; gene; ss; cancer; obesity; gastritis; diarrhoea; haemorrhoid;

XX Human; gene; ss; cancer; obesity; gastritis; diarrhoea; haemorrhoid;

KW asthma; anaemia; graft-versus-host reaction; allergic reaction;

KW cystic fibrosis; hypogonadism; cardiovascular disorder; arthritis;

KW osteoarthritis; arteriosclerosis; hypertension; bacterial infection;

KW

KW

KW

KW

XX

OS

XX

PN

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PD

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PF

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proriasis; diabetes mellitus; hepatitis; Alzheimer's disease;
Huntington's disease; Parkinson's disease; AIDS; tuberculosis;
viral infection; malaria; goiter; infertility; endometriosis;
muscular disorder.

Homo sapiens.

US2004121396-A1.

24-JUN-2004.

19-DEC-2003; 2003US-00741790.

14-JUN-1999; 99US-00333159.

29-JUN-1999; 99US-00342364.

10-SEP-1999; 99US-00393996.

19-OCT-1999; 99US-00420707.

07-JAN-2000; 2000US-00479249.

27-APR-2000; 2000US-00559497.

24-MAY-2000; 2000US-00578063.

16-JUN-2000; 2000US-00596194.

23-JUN-2000; 2000US-00602871.

30-JUN-2000; 2000US-00608452.

12-JAN-2001; 2001US-00759130.

(MILL-) MILLENNIUM PHARM INC.

Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;

Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;

WPI; 2004-479675/45.

New TANGO, INTERCEPT, and MANGO, useful in diagnosing, preventing, and

treating cancer, constipation, hemorrhoids, cystic fibrosis,

hypogonadism, psoriasis, hepatitis, Alzheimer's disease, AIDS,

tuberculosis, malaria, goiter, infertility.

Claim 2; SEQ ID NO 71; 483pp; English.

The invention relates to human polynucleotides and the polypeptides they

encode. The invention also relates to a host cell containing a

polynucleotide of the invention, an antibody which selectively binds with

a polypeptide of the invention, a method of detecting the presence of a

polypeptide in a sample, a method of identifying a compound which binds

with a polypeptide, and a method of modulating the activity of a

polypeptide. The polynucleotides, polypeptides and compositions are

useful for diagnosing, preventing and/or treating cancer, obesity,

gastritis, diarrhoea, haemorrhoids, asthma, anaemia, graft-versus-host

reactions, allergic reactions, cystic fibrosis, hypogonadism,

cardiovascular disorders, arthritis, osteoarthritis, arteriosclerosis,

hypertension, bacterial infections, psoriasis, diabetes mellitus,

hepatitis, Alzheimer's disease, Huntington's disease, Parkinson's

disease, AIDS, tuberculosis, viral infections, malaria, goiter,

infertility, endometriosis, wounds and muscular disorders. This sequence

represents a human polynucleotide of the invention. Note: The sequence

data for this patent did not form part of the printed specification but

was obtained in electronic format from USPTO at

seqdata.uspto.gov/sequence.html.

Sequence 3594 BP; 958 A; 810 C; 921 G; 905 T; 0 U; 0 Other;

Query Match 99.7%; Score 1459.8; DB 12; Length 3594;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACATCTAAGAATTATCCCGGACCTACCCCAATCACAATCTTTGCGAAAGACAATT 60

Db 228 ATGACATCTAAGAATTATCCCGGACCTACCCCAATCACAATCTTTGCGAAAGACAATT 287

QY 61 ACAGTACCAAGGGGAAAGACATGATTCGAGTTGGGAGATTTGATATCGAATCCAG 120

Db 288 ACAGTACCAAGGGGAAAGACATGATTCGAGTTGGGAGATTTGATATCGAATCCAG 347

QY 121 ACCTGCTCTTCTGATATCTTCTCTTCAACAGCTCTTTCAGATCAATATGTCATCTGT 180
DB 348 ACCTGCTCTTCTGATATCTTCTCTTCAACAGCTCTTTCAGATCAATATGTCATCTGT 407
QY 181 GGAAGTATGATCTTCCCAAGAACCTCTTCTGACACAAAGTGAAGTAAACCGTCCGCTTT 240
DB 408 GGAAGTATGATCTTCCCAAGAACCTCTTCTGACACAAAGTGAAGTAAACCGTCCGCTTT 467
QY 241 GAGAGTGGATCCCAATCTTCTGCGCGGGGTTTTTGTCTGACCTATGCGAGCAGCCAT 300
DB 468 GAGAGTGGATCCCAATCTTCTGCGCGGGGTTTTTGTCTGACCTATGCGAGCAGCCAT 527
QY 301 CCAGATTTAATAATCTTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATCAGCAAA 360
DB 528 CCAGATTTAATAATCTTTTGGAAACGAGCTAGCCATTTATTTGAAGACAGAAATCAGCAAA 587
QY 361 TTCTGCCCGAGCTGGTTGAGAGAGCTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 420
DB 588 TTCTGCCCGAGCTGGTTGAGAGAGCTAGCAGGAGACATTTCTGGGAATATGGTAGATGGA 647
QY 421 TATAGATACCTCTTTATTTGTCAAAAGCTGCCATCCATGCAGGAATAATTTGCTGATGAA 480
DB 648 TATAGATACCTCTTTATTTGTCAAAAGCTGCCATCCATGCAGGAATAATTTGCTGATGAA 707
QY 481 CTAGGTGGCAGATCAGTGTCTTTCAGCGCAAAAGGATCAGTCATATGAAGGATTTCTG 540
DB 708 CTAGGTGGCAGATCAGTGTCTTTCAGCGCAAAAGGATCAGTCATATGAAGGATTTCTG 767
QY 541 GCCAATGGTCTTTCTCGAGGATGGTTCCCTGTGCAGCAAGCATTTCTGTTTACCTCC 600
DB 768 GCCAATGGTCTTTCTCGAGGATGGTTCCCTGTGCAGCAAGCATTTCTGTTTACCTCC 827
QY 601 AATGGTTGCAGCAGATCCTTGAGTTTGAACCTGACCGGCAAAATCAGAGCTTCTTCTCTCA 660
DB 828 AATGGTTGCAGCAGATCCTTGAGTTTGAACCTGACCGGCAAAATCAGAGCTTCTTCTCTCA 887
QY 661 TGGCAGTGGTCAATGAGATGGAGACCAAGTTCACTGGTCTCTGCGCAAGCCCGACTT 720
DB 888 TGGCAGTGGTCAATGAGATGGAGACCAAGTTCACTGGTCTCTGCGCAAGCCCGACTT 947
QY 721 CAGGACCAAGCCCATCATGGCTTCGGCGCAGATGACACCAACCAACACAGAG 780
DB 948 CAGGACCAAGCCCATCATGGCTTCGGCGCAGATGACACCAACCAACACAGAG 1007
QY 781 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAAGGATCT 840
DB 1008 TGGCTGGAGATCGATTTGGGGGAGAAAAGAAAATAACAGGAATTAGGACCAAGGATCT 1067
QY 841 ACAGATCGAACTTCAACTTTTATGTTAAGAGTTTGTGATGAACTTCAAAAACAATAAT 900
DB 1068 ACAGATCGAACTTCAACTTTTATGTTAAGAGTTTGTGATGAACTTCAAAAACAATAAT 1127
QY 901 TCTAAGTGGAGACCTATTAAGGAATTTGTAATATGAAGAAAGGTTTTCAGGGTAAC 960
DB 1128 TCTAAGTGGAGACCTATTAAGGAATTTGTAATATGAAGAAAGGTTTTCAGGGTAAC 1187
QY 961 TCTAATCTTTCGGGACCCAGTGCAAAACAAATTTCTCCCTCCATCGTGGCCAGATATGTG 1020
DB 1188 TCTAATCTTTCGGGACCCAGTGCAAAACAAATTTCTCCCTCCATCGTGGCCAGATATGTG 1247
QY 1021 CGGTTGTTCCTCCAGACATGCGACAGAGGATAGCTTTGAAGGTGGAGCTCATTTGGTTGC 1080
DB 1248 CGGTTGTTCCTCCAGACATGCGACAGAGGATAGCTTTGAAGGTGGAGCTCATTTGGTTGC 1307
QY 1081 CAGATTACAGAGGTATGATTTCTATTTGGTGGCGCAGACAGTCAAGCACCAAGTGT 1140
DB 1308 CAGATTACAGAGGTATGATTTCTATTTGGTGGCGCAGACAGTCAAGCACCAAGTGT 1367
QY 1141 TCAACTAAGAAAGATGAGACAAATCAACAGGGCCATCCCTCTCGGAAGAAACATCCACA 1200
DB 1368 TCAACTAAGAAAGATGAGACAAATCAACAGGGCCATCCCTCTCGGAAGAAACATCCACA 1427
QY 1201 GGAATAAACATTACAAACGGTGGCTATTCCATTGGTGGTCTCTTGTCTGCTGTTGCT 1260

DB 1428 GGAATAAACATTACAAACGGTGGCTATTCCATTGGTGGTCTCTTGTCTGCTGTTGCT 1487
QY 1261 GGAATGGGATCTTTTCAGCCTTTAGAAAAGAAAGAAAGAAAGTCCGTATGGATCA 1320
DB 1488 GGAATGGGATCTTTTCAGCCTTTAGAAAAGAAAGAAAGTCCGTATGGATCA 1547
QY 1321 GCGAGGCTCAGAAAAACAGACTGTTGGAAGCAGATTAAATATATCCCTTTGCGCAGACATCAG 1380
DB 1548 GCGAGGCTCAGAAAAACAGACTGTTGGAAGCAGATTAAATATATCCCTTTGCGCAGACATCAG 1607
QY 1381 TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAAGTTAGATCTC 1440
DB 1608 TCAGCTGAGTTTACCATCAGCTATGATATGAGAGGAGATGACACAAAAGTTAGATCTC 1667
QY 1441 ATCAACAGTATATGCGAGGTTA 1463
DB 1668 ATCAACAGTATATGCGAGATT 1690

RESULT 15
ADL62155
ID ADL62155 standard; DNA; 3676 BP.
XX
AC ADL62155;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ovarian cancer DNA marker #20367.
XX
KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
OS Homo sapiens.
XX
PN WO200170979-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009126.
XX
PR 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lee J, Lillie J;
XX
DR WPI; 2001-611502/70.
XX
PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
XX
PS Disclosure; SEQ ID NO 20367; 106pp; English.
XX
CC The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a

marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

XX SQ Sequence 3676 BP; 967 A; 841 C; 953 G; 914 T; 0 U; 1 Other;

Query Match 99.7%; Score 1459.8; DB 5; Length 3676;

Best Local Similarity 99.94; Pred. No. 0; Matches 1461; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	ATGACATCTAAGAAATTATCCGGACCTACCCCAATCACACTGTTTGGCGAAAGACAAAT	60
DB	294	ATGACATCTAAGAAATTATCCGGACCTACCCCAATCACACTGTTTGGCGAAAGACAAAT	353
QY	61	ACAGTACCAAGGGGAAAGACTGATTCGAGTGGGAGATTGGATATCGAATCCCAG	120
DB	354	ACAGTACCAAGGGGAAAGACTGATTCGAGTGGGAGATTGGATATCGAATCCCAG	413
QY	121	ACCTGTGCTTCGACTATCTCTCTCCACAGCTCTTCAGATCAATATGCTCATCTGT	180
DB	414	ACCTGTGCTTCGACTATCTCTCTCCACAGCTCTTCAGATCAATATGCTCATCTGT	473
QY	181	GGAGTATGACTGTTCCTCAAGAACTCTTCTGCAACACAGTCAAGTCAACCGTCCGCTT	240
DB	474	GGAGTATGACTGTTCCTCAAGAACTCTTCTGCAACACAGTCAAGTCAACCGTCCGCTT	533
QY	241	GAGAGTGGATCCCAATTTCTGCGGGGTTTTTGTGACCTATCGAGCAGCGACCAT	300
DB	534	GAGAGTGGATCCCAATTTCTGCGGGGTTTTTGTGACCTATCGAGCAGCGACCAT	593
QY	301	CCAGATTTAATACATGTTTGGAAACGAGCTAGCCATTTTGAAGACAGATACAGCAA	360
DB	594	CCAGATTTAATACATGTTTGGAAACGAGCTAGCCATTTTGAAGACAGATACAGCAA	653
QY	361	TTCTGCCAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGTGA	420
DB	654	TTCTGCCAGCTGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGTGA	713
QY	421	TATAGAGATACCTTTTATTTGTCAAAGCTGCCATCCATCGAGGAATAATTTGCTGATGA	480
DB	714	TATAGAGATACCTTTTATTTGTCAAAGCTGCCATCCATCGAGGAATAATTTGCTGATGA	773
QY	481	CTAGTGGCCAGATCAGTGTGCTTCAGCCGAAGGGATCAGTCGATATGAAGGATCTG	540
DB	774	CTAGTGGCCAGATCAGTGTGCTTCAGCCGAAGGGATCAGTCGATATGAAGGATCTG	833
QY	541	GCCAAATGGTGTCTTTTCGAGGGATGTTCTCTGTGACAGAGCGATTTCTGTTTACTCC	600
DB	834	GCCAAATGGTGTCTTTTCGAGGGATGTTCTCTGTGACAGAGCGATTTCTGTTTACTCC	893
QY	601	AATGGTTGACGAGATCTTTGAGTTTGTAACTGACGGGCAATCAGAGCTTCTTCTCTCA	660
DB	894	AATGGTTGACGAGATCTTTGAGTTTGTAACTGACGGGCAATCAGAGCTTCTTCTCTCA	953
QY	661	TGGCAGTCGGTCAATCAGAGTGAGACCAAGTTTCACTGGTCTCTGGCCAGCCGACTT	720
DB	954	TGGCAGTCGGTCAATCAGAGTGAGACCAAGTTTCACTGGTCTCTGGCCAGCCGACTT	1013

QY	721	CAGGACCAAGGCCCATCATCGGCTTCGGCGCAGTAGCAACCAACCAACCAACCAAGAG	780
DB	1014	CAGGACCAAGGCCCATCATCGGCTTCGGCGCAGTAGCAACCAACCAACCAACCAAGAG	1073
QY	781	TGCTCGAGATCGATTTGGGGGAGAAAAAATAACAGGAATTAGGACCAAGGATCT	840
DB	1074	TGCTCGAGATCGATTTGGGGGAGAAAAAATAACAGGAATTAGGACCAAGGATCT	1133
QY	841	ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAATTTCAAAAACAATAAT	900
DB	1134	ACACAGTCGAACCTTCAACTTTTATGTTAAGAGTTTGTGATGAATTTCAAAAACAATAAT	1193
QY	901	TCTAAGTCGAAGACCTTATAAGGAAATTGTGAATAATGAAGAAAGGTTTTCAGGGTAAAC	960
DB	1194	TCTAAGTCGAAGACCTTATAAGGAAATTGTGAATAATGAAGAAAGGTTTTCAGGGTAAAC	1253
QY	961	TCTAATTTTCGGGACCCAGTGCAGAAACAATTTTCATCCCTCCCATCGTGGCCAGATATG	1020
DB	1254	TCTAATTTTCGGGACCCAGTGCAGAAACAATTTTCATCCCTCCCATCGTGGCCAGATATG	1313
QY	1021	CGGTTGTCTCCCGCAGACATGGCCACAGAGATAGCCTTGAAGGTGAGCTCATTTGTTGC	1080
DB	1314	CGGTTGTCTCCCGCAGACATGGCCACAGAGATAGCCTTGAAGGTGAGCTCATTTGTTGC	1373
QY	1081	CAGATTACACAAGGTAATGATTCAATTTGTTGGCGCAAGCAAGTCAAAGCACCAAGTGT	1140
DB	1374	CAGATTACACAAGGTAATGATTCAATTTGTTGGCGCAAGCAAGTCAAAGCACCAAGTGT	1433
QY	1141	TCAACTTAAGAAAGAGATGAGACAATCACAAGGCCCATCCCTCGGAAGAAACATCCACA	1200
DB	1434	TCAACTTAAGAAAGAGATGAGACAATCACAAGGCCCATCCCTCGGAAGAAACATCCACA	1493
QY	1201	GGATTAACAATTTACACCGTGGCTATTTCCATTGGTGTCTCTTGTCTCTGGTGTGTCT	1260
DB	1494	GGATTAACAATTTACACCGTGGCTATTTCCATTGGTGTCTCTTGTCTCTGGTGTGTCT	1553
QY	1261	GGATTTGGGATCTTTTCAGCCTTTAGAAAAGAAAGAAAGAAAGTCCGTATGGATCA	1320
DB	1554	GGATTTGGGATCTTTTCAGCCTTTAGAAAAGAAAGAAAGAAAGTCCGTATGGATCA	1613
QY	1321	GGGAGGCTCAGAAAAACAGACTGTTTGGAAAGCAGATTTAAATATCCCTTTGCCAGACATCAG	1380
DB	1614	GCAGAGGCTCAGAAAAACAGACTGTTTGGAAAGCAGATTTAAATATCCCTTTGCCAGACATCAG	1673
QY	1381	TCAGCTGAGTTTACCCTACGCTATGATATGAGAGGAGATGACACAAAAGTTAGATCTC	1440
DB	1674	TCAGCTGAGTTTACCCTACGCTATGATATGAGAGGAGATGACACAAAAGTTAGATCTC	1733
QY	1441	ATCACAAGTGTATATGGCAGTTA	1463
DB	1734	ATCACAAGTGTATATGGCAGTTA	1756

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